

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:33:05 ; Search time 1725.82 Seconds

(without alignments)  
1214.912 Million cell updates/sec

Title: US-09-380-682-2

Perfect score: 591

Sequence: 1 ATGCATGCAACGCTCCGGA.....AGTCATCATCCGACAA 591

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1219726 seqs, 1773875003 residues

Total number of hits satisfying chosen parameters: 24395452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents.NA:\*

1: /cgn2\_6/ptodata/2/pna/PCRNUS\_COMB.seq:\*

2: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq:\*

7: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq:\*

8: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq:\*

9: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq:\*

10: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq:\*

11: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq:\*

12: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq:\*

13: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq:\*

14: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq:\*

15: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq:\*

16: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq:\*

17: /cgn2\_6/ptodata/2/pna/US093\_COMB.seq:\*

18: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq:\*

19: /cgn2\_6/ptodata/2/pna/US095\_COMB.seq:\*

20: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq:\*

21: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq:\*

22: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq:\*

23: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq:\*

24: /cgn2\_6/ptodata/2/pna/US097\_COMB.seq:\*

25: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq:\*

26: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*

27: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*

28: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*

29: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*

30: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*

31: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*

32: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*

33: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*

34: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*

35: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*

36: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*

37: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*

38: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*

39: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*

40: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*

41: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*

42: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*

43: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	100.0	591	17	US-09-380-682-2
2	583	98.6	591	17	US-09-380-682-18
3	581.4	98.4	591	17	US-09-380-682-16
4	579.8	98.1	591	17	US-09-380-682-12
5	578.2	97.8	591	17	US-09-380-682-10
6	573.4	97.0	591	17	US-09-380-682-14
7	447.2	75.7	6801	5	US-08-126-505A-12
8	447.2	75.7	6951	14	US-09-023-655-1265
9	436.2	73.8	7028	18	US-09-471-275-1933
10	436.2	73.8	7028	18	US-09-496-914A-6567
11	431.2	73.0	574	48	US-60-234-446-1627
12	424.8	71.9	574	48	US-60-234-446-1612
13	406.8	68.8	6938	17	US-09-359-922-358
14	406.8	68.8	6938	17	US-09-359-922-357
15	270.4	45.8	837	24	US-09-716-475-3923
16	267.4	45.2	667	48	US-09-471-275-1975
17	252.6	42.7	398	18	US-60-234-446-1613
18	247.4	41.9	420	16	US-09-289-768-34927
19	239.8	40.6	391	19	US-09-515-128-19608
20	239.8	40.6	476	16	US-09-205-070-21958
21	239.8	40.6	476	17	US-09-340-623-21958
22	239.8	40.6	476	17	US-09-359-922-357
23	239.8	40.6	476	17	US-09-359-922-357
24	225	38.1	228	17	US-09-380-682-30
25	217	36.7	228	17	US-09-380-682-28
26	215.4	36.4	228	17	US-09-380-682-26
27	213.8	35.2	228	17	US-09-380-682-22
28	212.2	35.9	228	17	US-09-380-682-20
29	207.4	35.1	228	17	US-09-380-682-18
30	189.4	32.0	385	18	US-09-489-036-10281
31	177.2	30.0	550	22	US-60-234-446-16281
32	174.6	29.5	500	22	US-09-637-886-1326
33	168	28.4	630	42	US-60-177-507-1243
34	168	28.4	630	42	US-60-177-507-1243
35	166.8	28.2	467	39	US-60-147-499-18977
36	166.8	28.2	467	39	US-60-147-499-18977
37	166.2	28.1	470	17	US-09-353-690-4138
38	166.2	28.1	472	16	US-09-205-070-21959
39	166.2	28.1	472	17	US-09-340-623-21959
40	164.6	27.9	217	48	US-60-234-446-1625
41	164.6	27.9	217	48	US-60-234-446-1617
42	163	27.6	2644	48	US-60-234-446-4632
43	161	27.2	723	43	US-60-188-162-1554
44	161	27.2	723	43	US-60-188-162-1555
45	161	27.2	723	43	US-60-188-162-2514

#### ALIGNMENTS

```
RESULT 1
US-09-380-682-2
; Sequence 2, Application US/09380682
; GENERAL INFORMATION:
;   APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
;             COX, Vivienne Frances
;             SMITH, Richard Anthony Godwin
; TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE
; SEQUENCES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: FOLEY & LARDNER
;   STREET: 3000 K Street, N.W.
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20007-5109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/380,682
;   FILING DATE: 19-Oct-1999
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/GB98/00727
;   FILING DATE: 05-MAR-1998
;   APPLICATION NUMBER: GB 9704519.9
;   FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: ISACSON, John P.
;   REGISTRATION NUMBER: 33,715
;   REFERENCE/DOCKET NUMBER: 88362/107
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 672-5300
;   TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 591 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-380-682-2
```

```
Query Match      100.0%; Score 591; DB 17; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.2e-180;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGCAACGCTCGGAAATGCTGCGCGCCGACCAACTGACTGATGAA 60
   |||||||
DB 1 ATCCAGGCAACGCTCGGAAATGCTGCGCGCCGACCAACTGACTGATGAA 60

QY 61 TTGAGTCCGATCGGTACTGCTGAAGTACGAATGCGCGGGTTATACGGCGC 120
   |||||||
DB 61 TTGAGTCCGATCGGTACTGCTGAAGTACGAATGCGCGGGTTATACGGCGC 120

QY 121 CCGTTTCTATCATCTGCGCTGAAAACTGCTGAGCTGCTAAGACCGTTGCCGA 180
   |||||||
DB 121 CCGTTTCTATCATCTGCGCTGAAAACTGCTGAGCTGCTAAGACCGTTGCCGA 180

QY 181 CGTAAATCTGTGATATCCGCAAGATCCGGTTAAGGCGATGTCATGATCAAGGC 240
   |||||||
DB 181 CGTAAATCTGTGATATCCGCAAGATCCGGTTAAGGCGATGTCATGATCAAGGC 240

QY 241 ATCCAGTGGTCCCAATTAATATCTTGTACTAAGGTTACCGTGTGATGGTCC 300
   |||||||
DB 241 ATCCAGTGGTCCCAATTAATATCTTGTACTAAGGTTACCGTGTGATGGTCC 300
```

```
QY 301 TCCAGCGCTACATGATCTCTGTGATGATCTGCTATTTGGATAATGAACCGGATT 360
   |||||||
DB 301 TCCAGCGCTACATGATCTCTGTGATGATCTGCTATTTGGATAATGAACCGGATT 360

QY 361 TGTACCGAATTCGCTGCTGCGCGCGGACCATGCGCAACGGTGTTCACCTGATC 420
   |||||||
DB 361 TGTACCGAATTCGCTGCTGCGCGCGGACCATGCGCAACGGTGTTCACCTGATC 420

QY 421 AGTCGAGATATTTCTACTATGTTCTGTGTGATGACCTGCAATGCAATCGGTAGCCGT 480
   |||||||
DB 421 AGTCGAGATATTTCTACTATGTTCTGTGTGATGACCTGCAATGCAATCGGTAGCCGT 480

QY 481 GGTAAAAAGTGTGAGCTGCTGCGGTGAGCGCGTCCATCTACTGCACTAGCAAAAGAGAT 540
   |||||||
DB 481 GGTAAAAAGTGTGAGCTGCTGCGGTGAGCGCGTCCATCTACTGCACTAGCAAAAGAGAT 540

QY 541 CAAGTGGCATCTGGAGCGCGCGGACCGCATGATCATCTCCGAACAA 591
   |||||||
DB 541 CAAGTGGCATCTGGAGCGCGCGGACCGCATGATCATCTCCGAACAA 591
```

```
RESULT 2
US-09-380-682-18
; Sequence 18, Application US/09380682
; GENERAL INFORMATION:
;   APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
;             COX, Vivienne Frances
;             SMITH, Richard Anthony Godwin
; TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE
; SEQUENCES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: FOLEY & LARDNER
;   STREET: 3000 K Street, N.W.
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20007-5109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/380,682
;   FILING DATE: 19-Oct-1999
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/GB98/00727
;   FILING DATE: 05-MAR-1998
;   APPLICATION NUMBER: GB 9704519.9
;   FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: ISACSON, John P.
;   REGISTRATION NUMBER: 33,715
;   REFERENCE/DOCKET NUMBER: 88362/107
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 672-5300
;   TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 18:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 591 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-380-682-18
```

```
Query Match      98.6%; Score 583; DB 17; Length 591;
Best Local Similarity 99.2%; Pred. No. 4.6e-178;
Matches 586; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 ATGCAGTCAACGCTCCGGAATGGCTGCCCTTGGCGGCGCCGACCAACTGACTGATGAA 60
D 1 ATGCAGTCAACGCTCCGGAATGGCTGCCCTTGGCGGCGCCGACCAACTGACTGATGAA 60
QY 61 TTGAGTTCCTCCGATCGGTACTACTGACTGACTGACTGACTGACTGACTGACTGACTG 120
D 61 TTGAGTTCCTCCGATCGGTACTACTGACTGACTGACTGACTGACTGACTGACTGACTG 120
QY 121 CCGTTTCTATCATCTGCTGAAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
D 121 CCGTTTCTATCATCTGCTGAAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CGTAAATCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
D 181 CGTAAATCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATCCAGTTCGCTCCCAATTAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
D 241 ATCCAGTTCGCTCCCAATTAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
D 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 TGTGACCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
D 361 TGTGACCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AGTCGCGAGTATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
D 421 AGTCGCGAGTATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GGTAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
D 481 GGTAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 CAAGTGGGCACTGAGAGCGCGCGGACCGGACGAGTGCATCCCGAACA 591
D 541 CAAGTGGGCACTGAGAGCGCGCGGACCGGACGAGTGCATCCCGAACA 591

```

## RESULT 3

```

; Sequence 16, Application US/09380682
; GENERAL INFORMATION:
; APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
; COX, Vivienne Frances
; TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CRL)-LIKE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,682
; FILING DATE: 19-Oct-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB98/00727
; FILING DATE: 05-MAR-1998
; APPLICATION NUMBER: GB 9704519.9
; FILING DATE: 05-MAR-1997

```

```

ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOC NUMBER: 88362/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-380-682-16

```

```

Query Match 98.4%; Score 581.4; DB 17; Length 591;
Best Local Similarity 99.0%; Pred. No. 1.5e-177;
Matches 585; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 ATGCAGTCAACGCTCCGGAATGGCTGCCCTTGGCGGCGCCGACCAACTGACTGATGAA 60
D 1 ATGCAGTCAACGCTCCGGAATGGCTGCCCTTGGCGGCGCCGACCAACTGACTGATGAA 60
QY 61 TTGAGTTCCTCCGATCGGTACTACTGACTGACTGACTGACTGACTGACTGACTGACTG 120
D 61 TTGAGTTCCTCCGATCGGTACTACTGACTGACTGACTGACTGACTGACTGACTGACTG 120
QY 121 CCGTTTCTATCATCTGCTGAAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
D 121 CCGTTTCTATCATCTGCTGAAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CGTAAATCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
D 181 CGTAAATCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ATCCAGTTCGCTCCCAATTAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
D 241 ATCCAGTTCGCTCCCAATTAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
D 301 TCCAGGCTACATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 TGTGACCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
D 361 TGTGACCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AGTCGCGAGTATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
D 421 AGTCGCGAGTATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GGTAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
D 481 GGTAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 CAAGTGGGCACTGAGAGCGCGCGGACCGGACGAGTGCATCCCGAACA 591
D 541 CAAGTGGGCACTGAGAGCGCGCGGACCGGACGAGTGCATCCCGAACA 591

```

## RESULT 4

```

; Sequence 12, Application US/09380682
; GENERAL INFORMATION:
; APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
; COX, Vivienne Frances
; TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CRL)-LIKE
; NUMBER OF SEQUENCES: 64

```

## CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

## INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-380-682-12

Query Match 98.1%; Score 579.8; DB 17; Length 591;

Best Local Similarity 98.8%; Pred. No. 5e-177; Indels 0; Gaps 0;

Matches 584; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 421 ATCCGAGCAATTTTCACTATGTTCTGTGTGACCTACCTACCTGCAATCTGGTAGCCGT 480

Qy 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Db 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Qy 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

Db 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

## RESULT 5

US-09-380-682-10

Sequence 10, Application US/09380682

## GENERAL INFORMATION:

APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE

SEQUENCES

NUMBER OF SEQUENCES: 64

## CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-380-682-10

Query Match 97.8%; Score 578.2; DB 17; Length 591;

Best Local Similarity 98.6%; Pred. No. 1.6e-176; Indels 0; Gaps 0;

Matches 583; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 421 ATCCGAGCAATTTTCACTATGTTCTGTGTGACCTACCTACCTGCAATCTGGTAGCCGT 480

Qy 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Db 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Qy 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

Db 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

## RESULT 5

US-09-380-682-10

Sequence 10, Application US/09380682

## GENERAL INFORMATION:

APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE

SEQUENCES

NUMBER OF SEQUENCES: 64

## CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-380-682-10

Query Match 97.8%; Score 578.2; DB 17; Length 591;

Best Local Similarity 98.6%; Pred. No. 1.6e-176; Indels 0; Gaps 0;

Matches 583; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 421 ATCCGAGCAATTTTCACTATGTTCTGTGTGACCTACCTACCTGCAATCTGGTAGCCGT 480

Qy 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Db 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Qy 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

Db 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

## RESULT 5

US-09-380-682-10

Sequence 10, Application US/09380682

## GENERAL INFORMATION:

APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE

SEQUENCES

NUMBER OF SEQUENCES: 64

## CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-380-682-10

Query Match 97.8%; Score 578.2; DB 17; Length 591;

Best Local Similarity 98.6%; Pred. No. 1.6e-176; Indels 0; Gaps 0;

Matches 583; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 421 ATCCGAGCAATTTTCACTATGTTCTGTGTGACCTACCTACCTGCAATCTGGTAGCCGT 480

Qy 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Db 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Qy 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

Db 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

## RESULT 5

US-09-380-682-10

Sequence 10, Application US/09380682

## GENERAL INFORMATION:

APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE

SEQUENCES

NUMBER OF SEQUENCES: 64

## CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-380-682-10

Query Match 97.8%; Score 578.2; DB 17; Length 591;

Best Local Similarity 98.6%; Pred. No. 1.6e-176; Indels 0; Gaps 0;

Matches 583; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 421 ATCCGAGCAATTTTCACTATGTTCTGTGTGACCTACCTACCTGCAATCTGGTAGCCGT 480

Qy 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Db 481 GGTAAAAAGAGTTGAGCTGCTGGGTGAGCCCTCCATCTACTGCACTAGCAAAAGACAT 540

Qy 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

Db 541 CAAGTGGCATCTGGAGCGGCCGCCACCGCATGATCATCCCAACAA 591

## RESULT 5

US-09-380-682-10

Sequence 10, Application US/09380682

## GENERAL INFORMATION:

APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE

SEQUENCES

NUMBER OF SEQUENCES: 64

## CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: &lt;Unknown&gt;



```
|||||
Db 121 CGTTTCTATCATCTGCCTGAAAAACCTGCTGTGACGTCGTCAGGACGTTCCCA 180
Qy 181 CGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGATGGTGCATGTGATCAAGGC 240
Db 181 CGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGATGGTGCATGTGATCAAGGC 240
Qy 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGGTATACCGTGTGATGGTTC 300
Db 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGGTATACCGTGTGATGGTTC 300
Qy 301 TCCAGCGCTACATGATCATCTCTGTGATACATGTCATTGGATATGAACACCGATT 360
Db 301 TCCAGCGCTACATGATCATCTCTGTGATACATGTCATTGGATATGAACACCGATT 360
Qy 361 TGTGACCGAATTCGGTGTGTCGCCGCCAGCATCGCCACGGTATTCACCTATAC 420
Db 361 TGTGACCGAATTCGGTGTGTCGCCGCCAGCATCGCCACGGTATTCACCTATAC 420
Qy 421 ACTCGGATATTTTACATATGTTCTGTGTGATACCTACCATGCAATCGGTACCGT 480
Db 421 ACTCGGATATTTTACATATGTTCTGTGTGATACCTACCATGCAATCGGTACCGT 480
Qy 481 GGTAAAAAGTGTGAGTCCGTGGGTGAGCGGTCCATCATGCTACGTAGCAAGACGAT 540
Db 481 GGTCTGTAAGTGTGAGTCCGTGGGTGAGCGGTCCATCATGCTAGCTAGTATGAGAT 540
Qy 541 CAAGTGGGATCTGAGCGGCCGCCGACCGCATGTCATCCCGAACA 591
Db 541 CAAGTGGGATCTGAGCGGCCGCCGACCGCATGTCATCCCGAACA 591
```

RESULT 6  
US-09-380-682-14  
Sequence 14, Application US/09380682

GENERAL INFORMATION:

APPLICANT: MOSAKOWSKA, Danuta Ewa Irena

COX, Vivienne Frances

SMITH, Richard Anthony Godwin

TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,682

FILING DATE: 19-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/00727

FILING DATE: 05-MAR-1998

APPLICATION NUMBER: GB 9704519.9

FILING DATE: 05-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: ISACSON, John P.

REGISTRATION NUMBER: 33,715

REFERENCE/DOCKET NUMBER: 88362/107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-380-682-14

Query Match 97.0%; Score 573.4; DB 17; Length 591;  
Best Local Similarity 98.1%; Pred. No. 5.9e-175;  
Matches 580; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy 1 ATGCAAGTGAAGCTCCGGAATGCGTCCGTCGGCCGCCACCAACTGACTGATGA 60
Db 1 ATGCAAGTGAAGCTCCGGAATGCGTCCGTCGGCCGCCACCAACTGACTGATGA 60
Qy 61 TTGAGTTCCTGATGCTGCTGAAACTCTGTGTGAGTGTGCTAAGGACCGTTGCC 120
Db 61 TTGAGTTCCTGATGCTGCTGAAACTCTGTGTGAGTGTGCTAAGGACCGTTGCC 120
Qy 121 CGGTTTCTATCATCTGCCTGAAAACTGTGTGTGAGTGTGCTAAGGACCGTTGCC 180
Db 121 CGGTTTCTATCATCTGCCTGAAAACTGTGTGTGAGTGTGCTAAGGACCGTTGCC 180
Qy 181 CGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGATGGTGCATGTGATCAAGGC 240
Db 181 CGTAATCTTGTGTAATCCGCCAGATCCGGTTAACGGATGGTGCATGTGATCAAGGC 240
Qy 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGGTATACCGTGTGATGGTTC 300
Db 241 ATCCAGTTCGGTCCCAATTAATTTCTGTGACTAAAGGTATACCGTGTGATGGTTC 300
Qy 301 TCCAGCGCTACATGATCATCTCTGTGATACATGTCATTGGATATGAACACCGATT 360
Db 301 TCCAGCGCTACATGATCATCTCTGTGATACATGTCATTGGATATGAACACCGATT 360
Qy 361 TGTGACCGAATTCGGTGTGTCGCCGCCAGCATCGCCACGGTATTCACCTATAC 420
Db 361 TGTGACCGAATTCGGTGTGTCGCCGCCAGCATCGCCACGGTATTCACCTATAC 420
Qy 421 AGTCGGATATTTTACATATGTTCTGTGTGATACCTACCATGCAATCGGTACCGT 480
Db 421 AGTCGGATATTTTACATATGTTCTGTGTGATACCTACCATGCAATCGGTACCGT 480
Qy 481 GGTAAAAAGTGTGAGTCCGTGGGTGAGCGGTCCATCATGCTACGTAGCAAGACGAT 540
Db 481 GGTCTGTAAGTGTGAGTCCGTGGGTGAGCGGTCCATCATGCTAGCTAGTATGAGAT 540
Qy 541 CAAGTGGGATCTGAGCGGCCGCCGACCGCATGTCATCCCGAACA 591
Db 541 CAAGTGGGATCTGAGCGGCCGCCGACCGCATGTCATCCCGAACA 591
```

RESULT 7  
US-08-126-505A-12  
Sequence 12, Application US/08126505A

GENERAL INFORMATION:

APPLICANT: Atkinson, John P.

APPLICANT: Hourcade, Dennis

APPLICANT: Krzych, Malgorzata

TITLE OF INVENTION: Modified Truncated Complement System

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrice L. Babst

STREET: 2800 One Atlantic Center, 1201 West Peachtree

STREET: Street

CITY: Atlanta

STATE: Georgia

COUNTRY: US

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

```

/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/126,505A
/ FILING DATE: 24-SEP-1993
/ CLASSIFICATION: 435
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 07/695,514
/ FILING DATE: 03-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Padst, Patricia L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: WU101CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)873-8794
/ TELEFAX: (404)873-8795
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6801 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..5994
/
/ US-08-126-505A-12

```

```

Query Match          75.7%; Score 447.2; DB 5; Length 6801;
Best Local Similarity 85.0%; Pred. No. 1.4e-133;
Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```

```

QY 4 CAGTGCACGCTCCGGAATGCTGCGTGGCGGCGCCGACCAACTGACGATGATTT 63
DB 1 CAATGCAATGCCAGAAATGGCTTCATTTGCCAGGCTTACCACTACTAGATGATT 60
QY 64 GAGTCCCATGGTACCTACTGAATGCAATGCCCGGGTTATAGGGCGCCGCG 123
DB 61 GAGTTTCCCATGGGACATATCTGAATGATGATGATGATGATGATGATGATG 120
QY 124 TTTTCTATCATGCTGCTGAAATCTCTGCTGATGATGATGATGATGATGAT 183
DB 121 TTTTCTATCATGCTGCTGAAATCTCTGCTGATGATGATGATGATGATGAT 180
QY 184 AAATCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
DB 181 AAATCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 244 CAGTGCACGCTCCGGAATGCTGCGTGGCGGCGCCGACCAACTGACGATGATTT 303
DB 241 CAGTGCACGCTCCGGAATGCTGCGTGGCGGCGCCGACCAACTGACGATGATTT 300
QY 304 AGCGTATCATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
DB 301 TCTCCACATCATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 364 GACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 361 GACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 424 CGCAGATTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
DB 421 AGAGAGATTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 484 AAAAGGTGTTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
DB 481 AGAAGGTGTTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 544 GTGGGATCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 591
DB 541 GTGGGATCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 588

```

```

RESULT
8
US-09-023-655-1265
/ Sequence 1265, Application US/09023655
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ TITLE OF INVENTION: EXPRESSION
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 845-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1265:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6951 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: 930185
/
/ US-09-023-655-1265

```

```

Query Match          75.7%; Score 447.2; DB 14; Length 6951;
Best Local Similarity 85.0%; Pred. No. 1.4e-133;
Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```

```

QY 4 CAGTGCACGCTCCGGAATGCTGCGTGGCGGCGCCGACCAACTGACGATGATTT 63
DB 151 CAATGCAATGCCAGAAATGGCTTCATTTGCCAGGCTTACCACTACTAGATGATT 210
QY 64 GAGTCCCATGGTACCTACTGAATGCAATGCCCGGGTTATAGGGCGCCGCGCG 123
DB 211 GAGTTTCCCATGGGACATATCTGAATGATGATGATGATGATGATGATGATG 270
QY 124 TTTTCTATCATGCTGCTGAAATCTCTGCTGATGATGATGATGATGATGATGAT 183
DB 271 TTTTCTATCATGCTGCTGAAATCTCTGCTGATGATGATGATGATGATGATGAT 330
QY 184 AAATCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
DB 331 AAATCATGTGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
QY 244 CAGTGCACGCTCCGGAATGCTGCGTGGCGGCGCCGACCAACTGACGATGATTT 303

```

```

Db 391 CAGTCGGATCCCAATTAATATCTTGTACTAAGGATACCGACATTCATTGGTCTCG 450
QY 304 AGCGCTACATGCATCTCTGTGTGATCTGATCTATTGGGATTAATGAACACCGATTGT 363
Db 451 TCTGCCACATGCATCTCTGAGGTACTGATCTATTGGGATTAATGAACACCGATTGT 510
QY 364 GACCGAATCCCGATGCTGTGCGCGACCGACCATGCGCAAGGATGATTCACCTATGACGT 423
Db 511 GACGAAATTCCTTGTGGGCTACCCGCCACCATCAACCATGAGATTTTCTAGCACCAAC 570
QY 424 CCGGAGATTTTCACTATGCTGTGTGCTGACCTACCATCTGCAATCTGGGTAGCCGTGT 483
Db 571 AGAGAAATTTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 630
QY 484 AAAAGAGTGTTCAGCTGCTGGGTGAGCCGCTCATCTACTGCACTAGCAAAAGCATCAA 543
Db 631 AGAAAGTGTTCAGCTGCTGGGTGAGCCGCTCATCTACTGCACTAGCAAAAGCATCAA 690
QY 544 GTGGGATCTGAGCGCGCGCGACCGCATGATCATCCGAAACAA 591
Db 691 GTGGGATCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 738

```

## RESULT 9

```

US-09-471-275-1933
; Sequence 1933, Application US/09471275
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 782
; CURRENT APPLICATION NUMBER: US/09/471,275
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: pt_ct_genes Version 1.0
; SEQ ID NO 1933
; LENGTH: 7028
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(6148)
; OTHER INFORMATION: similar to g130186 in the genepept database release 114,
US-09-471-275-1933

```

```

Query Match 73.8%; Score 436.2; DB 18; Length 7028;
Best Local Similarity 84.9%; Pred. No. 5,2e-130;
Matches 500; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 4 CAGTGAACGCTCCGGAAT-GGCTGCCGTGCGGCCCGACCACTGATGATGAT 62
Db 151 caatgcaatgccccaaatgggtcttcatttcgcaagcctaccactaactatgagt 210
QY 63 TGAGTTCGCGATGGTACCTACCTGAACTAGAAATGCGCGGGTTAATAGCGCGCC 122
Db 211 tgaattcccatgggacatactgtaactgataatgacgagccggtatctcggaaagc 270
QY 123 GTTTTCTATCATCTGCTGAAAACCTCTGCTGATCTGCTGCTGCTGCTGCTGCTG 182
Db 271 gtctcatalcatctgcttaaaaaactcaagctgtaactgtaactgtaactgtaactg 330
QY 183 TAATCTTGCTGATATCCGCGCATCCGCTTAACGCGATGCTGATGATGATGATGAT 242
Db 331 taatacatgctgtaactccctccagatccctgtaactgtaactgtaactgtaactg 390
QY 243 CCAATTCGCTTCCCAATTAATATTTCTGTACTAAAGTTACCGTCTGATGATGAT 302
Db 391 ccagttcggatcccaataataataatcttgtaactaaagataccgactcattgttcctc 450
QY 303 CACGCTACATGCATCTCTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCTG 362
Db 451 gtctgcacatgcatcatctcagtgatcatctgcatctgcatctgcatctgcatctg 510
QY 363 TGACCGAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
Db 511 tgaagaatccctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 570
QY 423 TCGGAGATTTTCACTATGCTGTGTGATGATGATGATGATGATGATGATGATGATG 482
Db 571 cagagaagaatttcactatgatacagtgatgatacagtgatgatacagtgatgatac 630
QY 483 TAAAGAGTGTTCAGCTGCTGGGTGAGCCGCTCATCTACTGCACTAGCAAAAGCAT 542
Db 631 gagaagaagtgttgaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 690
QY 543 AGTGGCATCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 591
Db 691 agtggcatctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 738

RESULT 10
US-09-496-914A-6567
; Sequence 6567, Application US/09496914A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Suku, Ankura
; APPLICANT: Liu, Chenphua
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 787
; CURRENT APPLICATION NUMBER: US/09/496,914A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/353,690
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/431,517
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: US 09/328,351
; PRIOR FILING DATE: 1999-06-04

```

```

: PRIOR APPLICATION NUMBER: US 09/332,782
: PRIOR FILING DATE: 1999-06-14
: PRIOR APPLICATION NUMBER: US 09/235,076
: PRIOR FILING DATE: 1999-01-20
: PRIOR APPLICATION NUMBER: US 09/234,611
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: US 09/346,956
: PRIOR FILING DATE: 1999-07-02
: PRIOR APPLICATION NUMBER: US 09/362,510
: PRIOR FILING DATE: 1999-07-27
: PRIOR APPLICATION NUMBER: US 09/240,371
: PRIOR FILING DATE: 1999-01-29
: PRIOR APPLICATION NUMBER: US 09/248,797
: PRIOR FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: US 09/271,490
: PRIOR FILING DATE: 1999-03-18
: PRIOR APPLICATION NUMBER: US 09/293,972
: PRIOR FILING DATE: 1999-04-15
: PRIOR APPLICATION NUMBER: US 09/274,861
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: US 60/125,453
: PRIOR FILING DATE: 1999-03-19
: PRIOR APPLICATION NUMBER: US 60/126,605
: PRIOR FILING DATE: 1999-03-26
: PRIOR APPLICATION NUMBER: US 09/306,350
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: US 09/399,720
: PRIOR FILING DATE: 1999-09-21
: PRIOR APPLICATION NUMBER: US 09/404,284
: PRIOR FILING DATE: 1999-09-21
: PRIOR APPLICATION NUMBER: US 09/465,877
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
: NUMBER OF SEQ ID NOS: 10410
: SOFTWARE: PL CT genes Version 1.02
: SEQ ID NO 6567
: LENGTH: 7028
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (28)..(6148)
: OTHER INFORMATION: similar to g130186 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTX 3.3f00, default parameters
US-09-496-914A-6567
```

```

Query Match      73.8%; Score 436.2; DB 18; Length 7028;
Best Local Similarity 84.9%; Pred. No. 5.2e-130;
Matches 500; Conservative 0; Mismatches 88; Indels 1; Gaps 1;
```

```

QY 4 CAGTGAACGCTCCGGAAT-6GCTGCGGTGCGGCCCGGACCAACCTGATGATTT 62
DB 151 caatgaatgccccagaaatggcttccatttccagagccctaccacccaactgaaggtt 210
QY 63 TGAATCCCGATCGGTACTACTGAACTAGCAATCCGCCCGGGTTATAGCGGCCGCC 122
DB 211 tgaattcccatctggaaatatactgaacttgaatgcccgcctgttattccggaagacc 270
QY 123 GTTTTATCATCTGCTGAAAAACTCTGTGACTGAGTGGTGAAGGACCGTGGCCGAC 182
DB 271 gtttctatcatctgcttaaaaaactcagcttgactgtgttaagagcaaggtgcagagc 330
QY 183 TAAATCTGTGTAATCCGACAGATCCGGTTAAGGATGATGATGATGATGATGATGAT 242
DB 331 taatcaatgctgaatccctccagatccctggaatgcaatgcaatgcaatgcaatgcaat 390
QY 243 CCAATTCGATCCCAATTAATATCTGTACTAAAGGTTACCGTCTGATGATGATGAT 302
DB 391 ccaatctcgatcccaataataatattctgtactaaagataccgacatctgtgtctctc 450
QY 303 CAGCGCTACATCATCTCTGTGATGATGATGATGATGATGATGATGATGATGATG 362
```

```

DB 451 gcttcacacagcatcatcatctccagtgatacttctggaatggaataatgacactattg 510
QY 363 TACCGAATTCGGTGTGTCTGCGCCGACCATCGCAACGGTATTTACCTTATCAG 422
DB 511 tgacgaatctctgtggtacaccccccacacacacacacacacacacacacacacacac 570
QY 423 TCGCGATATTTTCTACTATGATGTTCTGTGTGACCTACACATGCAATCTGAGTACCG 482
DB 571 cagagagaatttctcatatgatacagtgatgacacacacacacacacacacacacacac 630
QY 483 TAAAGGTGTGAGTCGCGGCGGATCGGATCATCTGATGATGATGATGATGATGATGAT 542
DB 631 gagaagaagtgttgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 690
QY 543 AGTGGCATCTGGAGCGGCCCGGACCGCATGATCATCCGAACAA 591
DB 691 agtggcatctggagcggcccgccctcagtgatatacctaaca 739
```

## RESULT 11

```

US-60-234-446-1627
: Sequence 1627, Application US/60234446
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: FILE REFERENCE: CLO00832
: CURRENT APPLICATION NUMBER: US/60/234,446
: NUMBER OF SEQ ID NOS: 1797
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1627
: LENGTH: 574
: TYPE: DNA
: ORGANISM: HUMAN
US-60-234-446-1627
```

```

Query Match      73.0%; Score 431.2; DB 48; Length 574;
Best Local Similarity 84.6%; Pred. No. 8.2e-129;
Matches 484; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
```

```

QY 7 TGCACGCTCCGGAATGGCTGCGGTTCGCGCGCCGACCAACCTGATGATGATTTGAG 66
DB 2 tgaatgccccagaaatggcttccatttccagagccctaccacccaactgaaggttgcag 61
QY 67 TTCGGATCGGTACTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 126
DB 62 ttcccatggaatcatctcgaactatgaatgcaatgcaatgcaatgcaatgcaatgcaat 121
QY 127 TCTATATCTGCTGTAATAAATCTGTGTGATGATGATGATGATGATGATGATGATGAT 186
DB 122 tctatattctgtctaaataaactcagcttgatgcaatgcaatgcaatgcaatgcaatg 181
QY 187 TCTTGTGTAATCCGACAGATCCGGTTAAGGATGATGATGATGATGATGATGATGAT 246
DB 182 tcatgtcgaataccctccagatccctgtgaatgcaatgcaatgcaatgcaatgcaat 241
QY 247 TTCGGTCCCAATTAATATCTGTAATGATGATGATGATGATGATGATGATGATGATG 306
DB 242 ttggatcccaataataatattctgtcctaaagatacgcactcattgtgtctcgtc 301
QY 307 GCTACATGATATATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
DB 302 gcaacatgatacatctcagtgatactgtcatttggataataaacaacacattatgtgac 361
QY 367 CGAATTCGCTGCTGCTGCTGCGCCGACCATCGCAACGGTATGATGATGATGATGAT 426
DB 362 agaatctctgtggtctaccccccacacacacacacacacacacacacacacacacac 421
QY 427 GATATTTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
```



Tue Jan 16 09:11:51 2001

us-09-380-682-2.rnp

Page 10

```

1 GENERAL INFORMATION:
2 APPLICANT: Leshkowitz, Dena
3 APPLICANT: Liu, Jin
4 TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA
5 TITLE OF INVENTION: LIBRARIES
6 FILE REFERENCE: 20411-752CON1
7 CURRENT APPLICATION NUMBER: US/09/359,922A
8 CURRENT FILING DATE: 1999-07-22
9 EARLIER APPLICATION NUMBER: US 09/205,155
10 EARLIER FILING DATE: 1998-12-03
11 EARLIER APPLICATION NUMBER: US 09/034,341
12 EARLIER FILING DATE: 1998-02-13
13 NUMBER OF SEQ ID NOS: 13203
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO 358
16 LENGTH: 6938
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 US-09-359-922-358

```

Query Match	68.8%;	Score 406.8;	DB 17;	Length 6938;
Best Local Similarity	83.8%;	Pred. No. 1.8e-120;		
Matches 496;	Conservative	0;	Mismatches 92;	Indels 4;
				Gaps 3

OY	4	CAGCGAAGCGCTGGGAATGGCTGCGCTTGGCGGCCCGACCAACCGTACTATTAAT	63
Db	226	caatgaataagctccggaaatggcttcacatttgcgcagccctacaactaactatgtagcttc	285
OY	64	GAATTCCCGATGGGTACCTACCTGAGACACAGAAATCCGCCCC -GGTTATAGCGGCCGCC	122
Db	286	gaattcccatctgggaacatctcgaacttgaatgcgcgcctgggtattcttcggaaagcc	345
OY	123	GTTTTCATCATCTCCCTGAAAAACTCTGTCTGGACTGGTCTAAGACCGTTGGCGACG	182
Db	346	gtttctatcatcttccctaaanaactcagctcgcgacttggctaaaggaacaggttcagacg	405
OY	183	TAAATTTGTCATATCC -GCCAGATCCGGTTAACGG -CATGTGGCAGTGTATGAAG	239
Db	406	tcaatcatgtctaatccctcccgatccctcgtgaatggcattggcacatgtagtcaaga	465
OY	240	CATCCAGTTCGGGTCCCAATTAATATCTGTGACTGAAGAGTAAACCGTCCGTGATGGTTC	299
Db	466	catccagttccgatactccaataataatctctgtactaaagataacccgactcatttggctc	525
OY	300	CTCCAGCGCTAAATGCATCATCTCTGGTATACTGTCAATTGGGANTAAAGAACCCAT	359
Db	526	ctcgctcgcacatgcacatcctgaatgtagtcttgcatttggataaagaacaccocat	585
OY	360	TTGTGACCGAATTCGGTGTGCTGCGCGGACCATGCGCAACGGTGATTTCACCTAT	419
Db	586	ttgtgacgaataatctcttcttggctacccccccacacacacatgaatttcaatgaac	645
OY	420	CAGCGCGAGTTATTTACATCTGTGTTGTGGTGACCTACACACGCAATCTGGGTAGCG	479
Db	646	caaaagagagaatttctacttgcatacagtggtgacctaacgcgtcaatccctggaagcgg	705
OY	480	TGGTAAAGAGGTTTGGAGCTGTGGGTGAGCGGCTGCATACAGCACTGACCTGCAAGAGGA	539
Db	706	agggagagaagtggtttagctctgttggtyggccctccatataacgcacccgaatgagga	765
OY	540	TCAAAGTGGCATTGTGAGCGGCCGCGACCGCAGATGCATATCCGCAGAA	591
Db	766	tcaagtgtgcatcttgagcggcccccgcctctcgtgcatttactactaa	817

RESULT 15  
US-09-716-475-3923  
; Sequence 3923, Application US/09716475

; APPLICANT: Shyjan, Andrew W.  
 ; APPLICANT: MacBeth, Kyle J.  
 ; APPLICANT: Vasicek, Thomas

```

1  ? TITLE OF INVENTION: NOVEL NOCLEIC ACID MOLECULES AND USES
2  ? TITLE OF INVENTION: THEREFOR
3  ? FILE REFERENCE: 1600.2037-001
4  ? CURRENT APPLICATION NUMBER: US/09/716,475
5  ? CURRENT FILING DATE: 2000-11-20
6  ? PRIOR APPLICATION NUMBER: 60/166,506
7  ? PRIOR FILING DATE: 1998-11-19
8  ? NUMBER OF SEQ ID NOS: 8194
9  ? SOFTWARE: FASTSEQ FOR Windows Version 4.0
10 ? SEQ ID NO 3923
11 ? LENGTH: 837
12 ? TYPE: DNA
13 ? ORGANISM: Homo sapiens
14 ? FEATURE:
15 ? NAME/KEY: misc.feature
16 ? LOCATION: (1) ..(837)
17 ? OTHER INFORMATION: n = A,T,C or G
18 ? US-09-716-475-3923

```

Query Match	45.88;	Score 270.4;	DB 24;	Length 837;
Best Local Similarity	85.5%;	Pred. No. 1.4e-76;		
Matches 312; Conservative	0;	Mismatches 52;	Indels 1;	Gaps 1.

QY 4 CAGTGGAAAGCGTCGGATGGCTGGCGGTGGCGGCGCGAGCAACACTGGATGATGAATT 63  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 138 caatgaatagcccgcgaatggtc-ttaattgccaagcctacaactactactgtgaattc 196  
QY 64 GAGTTCGCAGTGGGACCTACAGCACTACGAAATACGCCGCCGGGTATAGCGCCGCCG 123  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 197 gagttcccatcttggaacatactcgaactatgagtgcgcctctgtattccggaaagaccg 256  
QY 124 TTTTTCATATGTGGCGTGGAAAACTGTCTGTCTGTGGATGGTGTGAAGAGACGGTGGCCGAGT 183  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 257 ttctcatcatcttgccataaaaaactcagctcgtgactggtgtcctaagcagcgtgcgaagct 316  
QY 184 AAATCTGTGCACAAACCGCCGAGATCCGGTAAACGGATACGGATACGATGATGAAAGCAATC 243  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 317 aaatcattgcgcgaatcccccacgaatccctcgtgacatgacatgcatgcatcaaaagcacc 376  
QY 244 CAGTGTGGTTCCTCCAAATTAATATTTTGTACTAAAGTAAAGCTGTGATGGTCTCCACC 303  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 377 cagttcggatcccaatataatatactctcgtacacaaagatcacgcgaactcatttggctcccg 436  
QY 304 AGCGCTACATGCATATCTCTGGTGTACTGTGCATTTTGGATATATGAACACCGGATTTGT 363  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 437 tctgcacacatcatctccagttgatacttgnattctgggataatgaaacacctattgtc 496  
QY 364 GACCG 368  
| | | | |  
Db 497 gacag 501

Search completed: January 13, 2001, 13:41:06  
Job time: 4081 sec



**THIS PAGE BLANK (uspto)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:32:20 ; Search time 85.47 Seconds  
(without alignments)  
2597.597 Million cell updates/sec

Title: US-09-380-682-2  
Sequence: 1 ATGCAGTGCACGCTCCCGA.....AGTGATCATCCCGACAA 591

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues  
Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_36: \*  
1: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1980.DAT: \*  
2: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1981.DAT: \*  
3: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1982.DAT: \*  
4: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1983.DAT: \*  
5: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1984.DAT: \*  
6: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1985.DAT: \*  
7: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1986.DAT: \*  
8: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1987.DAT: \*  
9: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1988.DAT: \*  
10: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1989.DAT: \*  
11: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1990.DAT: \*  
12: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1991.DAT: \*  
13: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1992.DAT: \*  
14: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1993.DAT: \*  
15: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1994.DAT: \*  
16: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1995.DAT: \*  
17: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1996.DAT: \*  
18: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1997.DAT: \*  
19: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1998.DAT: \*  
20: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1999.DAT: \*  
21: /cgn2\_2/gcgdata/geneseq/geneseqn/NA2000.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	100.0	591	19	V53262 Complement recepto
2	583	98.6	591	19	V53273 Complement recepto
3	581.4	98.4	591	19	V53272 Complement recepto
4	579.8	98.1	591	19	V53270 Complement recepto
5	578.2	97.8	591	19	V53269 Complement recepto
6	573.4	97.0	591	19	V53271 Complement recepto
7	447.2	75.7	6951	10	N91477 CRI protein DNA.
8	447.2	75.7	6951	12	O11642 Entire human comp
9	447.2	75.7	6951	20	Z38150 Human C3b/C4b rece
10	443.2	75.0	6951	14	O41867 CRI coding region.
11	327.2	55.4	5420	12	O11643 Partial human comp
12	327.2	55.4	5420	20	Z38151 Human C3b/C4b rece

13	225	38.1	228	19	V53279 Complement recepto
14	217	36.7	228	19	V53278 Complement recepto
15	215.4	36.4	228	19	V53277 Complement recepto
16	213.8	36.2	228	19	V53275 Complement recepto
17	212.2	35.9	228	19	V53274 Complement recepto
18	207.4	35.1	228	19	V53276 Complement recepto
19	63.4	10.7	3331	20	X84434 pB66-01, containi
20	61.2	10.4	74	19	V53285 Complement recepto
21	59.8	10.1	3337	12	O10989 B lymphocyte membr
22	56	9.5	1365	18	T61098 DNA encoding porci
23	56	9.5	1365	20	Z09145 MCP cDNA. Unident
24	50	8.5	50	19	V53263 Complement recepto
25	47.8	8.1	125	19	X11827 Human diallelic po
26	47	8.0	47	19	V53264 Complement recepto
27	45.2	7.6	50	19	V53286 Complement recepto
28	44.6	7.5	1146	20	V08935 DAF protein coding
29	44.6	7.5	1493	20	X87915 Human tumour assoc
30	44.6	7.5	1878	17	T46065 Membrane co-factor
31	44.6	7.5	2015	8	N70047 Encodes human deca
32	44.6	7.5	2096	16	O99105 Human DAF cDNA. H
33	44.6	7.5	2096	18	T84471 Human CD55 tumour
34	44.6	7.5	2102	20	X87914 Decay accelerating
35	44.6	7.5	2115	10	N91043 CDNA encoding a mo
36	44.6	7.5	2115	16	O79863 CD46 construct sub
37	44.6	7.5	2233	8	N70048 Membrane cofactor
38	44.6	7.5	2233	10	N91044 Decay accelerating
39	44.6	7.5	2233	16	O79864 Human glycopospha
40	44.6	7.5	2237	18	T90287 CDNA encoding a mo
41	43.4	7.3	2026	19	V09901 CD46 construct sub
42	43	7.3	1134	17	T17598 Membrane cofactor
43	43	7.3	1134	17	T17596 rsmcp cDNA SEQ ID
44	38.2	6.5	756	14	O46164
45	38.2	6.5	837	19	V40047

#### ALIGNMENTS

RESULT 1	
V53262	V53262 standard; DNA; 591 BP.
XX	
AC	V53262;
DT	18-JAN-1999 (first entry)
XX	
DE	Complement receptor type 1-like sequence CM7 DNA.
XX	
KW	Complement receptor type-1; CRI, CM7; complement; inhibitor;
KW	anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW	xenograft rejection; inflammation; Crohn's disease; asthma;
KW	pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW	autoimmune disease; rheumatoid arthritis; proliferative nephritis;
XX	myasthenia gravis; reproductive disorder; therapy; ss.
OS	Homo sapiens.
OS	Synthetic.
PN	W09839433-A1.
XX	
PD	11-SEP-1998.
XX	
PF	05-MAR-1998; 98MO-GB00727.
XX	
PR	05-MAR-1997; 97GB-0004519.
XX	
PA	(ADPR-) ADPROTECH PLC.
XX	
PI	Cox VF, Mossakowska DEI, Smith RAG;
XX	WPI: 1998-506358/43.
DR	P-PSDB; W79236.
XX	



Query Match 98.6%; Score 583; DB 19; Length 591;  
 Best Local Similarity 99.2%; Pred. No. 6e-188;  
 Matches 586; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 ATGCAGTCAACGCTCCGGAATGGCTCGCTGCGCGCCGACCAACTGACTGATGAA 60
   |||||||
Db 1 atgcagtgcaacgctccggaaatggctcgctgcgcgccgacacacccgactgataa 60
QY 61 TTTCAGTTCCTGATCGGTAATCCGAGATCGGTAATCCGAGATCGGTAATCCG 120
   |||||||
Db 61 tttagagttccctgatacgtacctaactgaactgaatgacgagccggttataagcgcgc 120
QY 121 CCGTTTCTCATCTGCTGTAAGAACTGCTGTAAGTGGTGTAGGACCGCTTGGCGA 180
   |||||||
Db 121 cggtttctcatctgctgtaagaaactgctgtaagtggtgtaggaacgcttgcgga 180
QY 181 CGTAATCTGTTGTAATCCGAGATCGGTAATCCGAGATCGGTAATCCGAGATCG 240
   |||||||
Db 181 cgtaaatcttgctgtaacccgagatccggttaacgagatgcatgatacaaggc 240
QY 241 ATCCAGTTCGTTCCCAATTAATATCTGTAAGGTTACGTTGATGTTCC 300
   |||||||
Db 241 atccagttcgtttcccaataataatcttgtaaggttacccgtctgattgttcc 300
QY 301 TCCAGCGCTACATGATCATCTGTAAGTGTGATGATGATGATGATGATGATGAT 360
   |||||||
Db 301 tccagcgctacatgatacatctctgtaagtgatgatacttgggataatgaacccgatt 360
QY 361 TGTGACCGAATTCGTTGCTGCTGCGCGACCAATCCGAGATCGGTAATCCG 420
   |||||||
Db 361 tgtgacccaatctcgttgcgtgctgctgcgcgacccaacggttgcattcatctacc 420
QY 421 AGTCGCGAGTAATTTTCTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
   |||||||
Db 421 aatcgcgagaatatttctactatgcttgcgttgcgttgcgttgcgttgcgttgcgt 480
QY 481 GGTAAAGAGTGTGTTGAGTGTGTTGAGTGTGTTGAGTGTGTTGAGTGTGTTG 540
   |||||||
Db 481 ggtaaaaagtgcttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 540
QY 541 CAAAGTGGCATCTGAGAGCGCGCGACCGACCGACGATGATGATGATGATGATG 591
   |||||||
Db 541 caagtgagcatctgagagcgcgcgacccgacgagtgatcatctccgaacaaa 591
  
```

RESULT 3  
 ID V53272 standard; DNA; 591 BP.  
 AC V53272;  
 DT 18-JAN-1999 (first entry)  
 DE Complement receptor type 1-like sequence CMS DNA.  
 XX  
 KW Complement receptor type-1; CRI; CMS; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy; ss.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN MO9839433-A1.  
 PD 11-SEP-1998.  
 PF 05-MAR-1998; 98WO-GB00727.  
 PR 05-MAR-1997; 97GB-0004519.

(ADPR-) ADPROTECH PLC.  
 PA Cox VE, Mossakowska DEI, Smith RAG;  
 PI WPI; 1998-506358/43.  
 DR P-PSDB; W79240.  
 XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PT used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 PS Claim 22; Page 47; 67pp; English.

This DNA sequence encodes CMS (see W79240), a protein that consists of the short consensus repeats (SCR) 1 and 2 from complement receptor type 1 (CRI) fused to an SCR3 (see W79245) in which 5 amino acids were altered to those found in the SCR3 of the CRI-like pseudogene (Cripse) putative product. CMS DNA was constructed by site-directed mutagenesis (see V53264-65) of pda103-5, which codes for SCR1-3 of CRI. pProcCRI-3CMS carrying CMS DNA was used to transform *Escherichia coli* BL21(DE3), and CMS was purified from solubilised inclusion bodies. The invention provides DNA sequences (see V53262 and V53269-79) encoding novel soluble engineered CRI polypeptides (see W53236-47) such as CMS that act as complement inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or disorder associated with inflammation or inappropriate complement activation, such as neurological disorders (e.g. multiple sclerosis and Parkinson's disease), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection), inflammatory disorders (e.g. Crohn's disease, asthma, and acute pancreatitis), post-ischaemic reperfusion conditions, infection or sepsis, immune complex disorders and autoimmune diseases (e.g. rheumatoid arthritis, proliferative nephritis and myasthenia gravis), and reproductive disorders.

Sequence 591 BP; 128 A; 160 C; 151 G; 152 T; 0 other;

Query Match 98.4%; Score 581.4; DB 19; Length 591;  
 Best Local Similarity 99.0%; Pred. No. 2.1e-187;  
 Matches 585; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY 1 ATGCAGTCAACGCTCCGGAATGGCTCGCTGCGCGCCGACCAACTGACTGATGAA 60
   |||||||
Db 1 atgcagtgcaacgctccggaaatggctcgctgcgcgccgacacacccgactgataa 60
QY 61 TTTCAGTTCCTGATCGGTAATCCGAGATCGGTAATCCGAGATCGGTAATCCG 120
   |||||||
Db 61 tttagagttccctgatacgtacctaactgaactgaatgacgagccggttataagcgcgc 120
QY 121 CCGTTTCTCATCTGCTGTAAGAACTGCTGTAAGTGGTGTAGGACCGCTTGGCGA 180
   |||||||
Db 121 cggtttctcatctgctgtaagaaactgctgtaagtggtgtaggaacgcttgcgga 180
QY 181 CGTAATCTGTTGTAATCCGAGATCGGTAATCCGAGATCGGTAATCCGAGATCG 240
   |||||||
Db 181 cgtaaatcttgctgtaacccgagatccggttaacgagatgcatgatacaaggc 240
QY 241 ATCCAGTTCGTTCCCAATTAATATCTGTAAGGTTACGTTGATGTTCC 300
   |||||||
Db 241 atccagttcgtttcccaataataatcttgtaaggttacccgtctgattgttcc 300
QY 301 TCCAGCGCTACATGATCATCTGTAAGTGTGATGATGATGATGATGATGATGATGAT 360
   |||||||
Db 301 tccagcgctacatgatacatctctgtaagtgatgatacttgggataatgaacccgatt 360
QY 361 TGTGACCGAATTCGTTGCTGCTGCGCGACCAATCCGAGATCGGTAATCCG 420
   |||||||
Db 361 tgtgacccaatctcgttgcgtgctgctgcgcgacccaacggttgcattcatctacc 420
QY 421 AGTCGCGAGTAATTTTCTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
   |||||||
  
```

D	b	421	agtcgcgagatcatttcaacatgatgtctcgtytgtagactaacgcgtcatccggtagcggt
O	y	481	GATAAAGGCTGGTTTACGTGGTGSGGTGAGCCGCCTGCCATCTCATTCAGCAAAAGCAGT
D	b	481	ggtcgtaagtgtttgagctcgtgtyggagccggtaccatactctcagctaggcaagaagat
O	y	541	CAGTGGCGCATCTGAGAGCGGCCCGSCGCCGACTGCATCATCCGAACAAG 591
D	b	541	caatgtggcatctcgagcggccgcgcagccagtcgatacctccgaacaag 591
R	E	SU	RESULT 4
V	I	3270	V53270 standard; DNA; 591 BP.
A	C	V53270:	
D	T	18-JAN-1999	(first entry)
D	E	Complement receptor type 1-like sequence CM2 DNA.	
K	M	Complement receptor type-1; CR1; CM2; complement; inhibitor;	
K	M	anti-hemolytic; multiple sclerosis; Parkinson's disease;	
K	M	xenograft rejection; inflammation; Crohn's disease; asthma;	
K	M	pancreatitis; post-ischemic reperfusion; infection; sepsis;	
K	M	autoimmune disease; rheumatoid arthritis; proliferative nephritis;	
K	M	myasthenia gravis; reproductive disorder; therapy; ss.	
H	M	Homo sapiens.	
O	S	Synthetic.	
X	X	WO9839433-A1.	
P	N	11-SEP-1998.	
P	D	05-MAR-1998; 98WO-GB00727.	
P	E	05-MAR-1998; 98WO-GB00727.	
P	R	05-MAR-1997; 97GB-0004519.	
P	A	(ADPR-) ADPTECH PLC.	
P	I	Cox VF, Mossakowska DEI, Smith RAG;	
X	X	WPI: 1998-506358/43.	
D	R	P-PSDB; W79238.	
P	T	Soluble polypeptide comprising short consensus repeats from LHR-A -	
P	T	used to treat disorders and diseases associated with inflammation or	
P	T	inappropriate complement activation	
X	X	Claim 22: Page 45; 67pp; English.	
X	X	This DNA sequence encodes CM2 (see W79238), a protein that consists	
C	C	of the short consensus repeats (SCR) 1 and 2 from complement	
C	C	receptor type 1 (CR1) fused to an SCR3 (see W79243) in which 4 amino	
C	C	acids were altered to those found in the SCR3 of the CR1-like	
C	C	peptidase (C1rps) putative product. CM2 DNA was constructed by	
C	C	site-directed mutagenesis (see V53264) of plasmid pBl013-5, which	
C	C	codes for SCR1-3 of CRI. pProcSCR1-CM2 carrying CM2 DNA was used	
C	C	to transform Escherichia coli BL21(DE3), and CM2 was purified from	
C	C	solubilized inclusion bodies. The invention provides DNA sequences	
C	C	(see V53262 and V53269-79) encoding novel soluble engineered CR1	
C	C	polypeptides (see W53236-47) such as CM2 that act as complement	
C	C	inhibitors with functional complement inhibition, including	
C	C	anti-hemolytic activity. These can be used to treat a disease or	
C	C	disorder associated with inflammation or inappropriate complement	
C	C	activation, such as neurological disorders (e.g., multiple sclerosis	
C	C	and Parkinson's disease), disorders of inappropriate or undesirable	
C	C	complement activation (e.g., xenograft rejection), inflammatory	
C	C	disorders (e.g., Crohn's disease, asthma, and acute pancreatitis),	
C	C	post-ischemic reperfusion conditions, infection or sepsis,	
C	C	immune complex disorders and autoimmune diseases (e.g., Rheumatoid	
C	C	arthritis, proliferative nephritis and myasthenia gravis), and	

CC	reproductive disorders.
XX	Sequence 591 BP; 134 A; 158 C; 146 G; 153 T; 0 other;
SO	Query Match 98.1%; Score 579.0; DB 19; Length 591; Best Local Similarity 98.8%; Pred. No. 7,3e-187; Matches 584; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	1 ATCAGTGCACAGCTCCGGAATGGCTGGCTTCGCGCGCCGACCAACTGACTGATGAA 60
DB	1 atcgagtcgaacgctccggaatgctgcgcttcgcgcgcgcgaccaaactgactgaa 60
QY	61 TTGTGAGTTCGGATCGGATACCTACCTGACAAACAAATGCGCCGGATTATAGCGCCG 120
DB	61 ttgtgagttccgagtcggtacccaccctgacaaagaaatgcccgcggtatagcgccg 120
QY	121 CGGTTTTATCATCTGCTGAAAAAAGCTGTGTGAGACGAGTGATGAAAGCGTTGGCA 180
DB	121 cggtttctatcatctgcctgaaaaaactctgctgactggtggtcaagacgcttgccga 180
QY	181 CGTAATCTCTGCTAATCCGCCAGATCCGGTTAAGCGCATGSGTCATGTATCAAAAGC 240
DB	181 cgtaaatctctgctaaatccgcacagctccggttaacggaatggtgcaatgataaaggc 240
QY	241 ATCCAGTTCGGTCCCAATTTAAATTTCTTGACTTAAAGTTACCGTCTGATTGGTTCC 300
DB	241 atccagttcggttcccaaatlaaataatcttctgactaaagttacgcgtctgattgcttc 300
QY	301 TCCAGGCGTACATCATCATCTCTGGTATGATCTGCTATTGGGATTAAGAACCAGATT 360
DB	301 tccagcgctacatcatcatctctggtatgactctgattggtgataatgaacaacgatt 360
QY	361 TGTGACCGAATTCGGTGTGGTGCGCGCGACATGCGCAAGGATGATTGACTGTATC 420
DB	361 tgtgaccgaatctcggtgtgtctgcgcgcgcctcccaaaaggtattcatctccacc 420
QY	421 AGTCGGGAGTATTTCCTACTATGAGTCTGTGTGATGACCTACACTGCATCTGGGTAACCGT 480
DB	421 aatcgcggaatcttccactatgctctgtgtgtagccacacacatgcaatctggttagccgt 480
QY	481 GGTAAAAAGGTGTGAGCTGCGGGGTAGAGCGGTCATCTACTGCACTAGCAAAAGACGAT 540
DB	481 ggtaaaaaggtgttgagctgctggtgtgtagccgctccatctgcaactagaaatgacgat 540
QY	541 CAAGTGGCATCTGGAGCGGCCCGGACCGAGCATGCATCCGCCGAATAA 591
DB	541 caagtggcatctggagcggcccgagacagtgacatcatccgacaataa 591
RESULT	5
V53269	V53269 standard; DNA; 591 BP.
XX	V53269;
XX	18-JAN-1999 (first entry)
DE	Complement receptor type 1-like sequence CMI DNA.
XX	Complement receptor type-1; CRI; CMI; complement; inhibitor;
KW	anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW	xenograft rejection; inflammation; Crohn's disease; asthma;
KW	pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW	autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW	myasthenia gravis; reproductive disorder; therapy; ss.
XX	Homo sapiens.
OS	Synthetic.
PM	W09839433-A1.
PD	11-SEP-1998.

PF	05-MAR-1998;	98WO-GB00727.
XX		
PR	05-MAR-1997;	97GB-0004519.
XX		
PA	(ADPR-) ADPROTECH PLC.	
PI	Cox VF, Mossakowska DEL, Smith RAG;	
XX		
DR	WPI: 1998-506358/43.	
DR	P-PSDB: W79237.	
XX		
PT	Soluble polypeptide comprising short consensus repeats from LHR-A -	
PT	used to treat disorders and diseases associated with inflammation or	
PT	inappropriate complement activation	
PS	Claim 22; Page 44; 67pp: English.	
XX		
CC	This DNA sequence encodes CMI (see W79237), a protein that consists	
CC	of the short consensus repeats (SCR) 1 and 2 from complement	
CC	receptor type 1 (CRI) fused to an SCR3 (see W79242) in which 5 amino	
CC	acids were altered to those found in the SCR3 of the CRI-like	
CC	pseudogene (CrIsse) putative product. CMI DNA was constructed by	
CC	site-directed mutagenesis (see W53265) of plasmid pDB1013-5, which	
CC	codes for SCR1-3 of CRI. pBIOESCRI-3CMI carrying CMI DNA was used	
CC	to transform Escherichia coli BL21(DE3), and CMI was purified from	
CC	solubilized inclusion bodies. The invention provides DNA sequences	
CC	(see W53262 and W53269-79) encoding novel soluble engineered CRI	
CC	polypeptides (see W53236-47) such as CMI that act as complement	
CC	inhibitors with functional complement inhibitory, including	
CC	anti-thrombotic, activity. These can be used to treat a disease or	
CC	disorder associated with inflammation or inappropriate complement	
CC	activation, such as neurological disorders (e.g. multiple sclerosis	
CC	and Parkinson's disease), disorders of inappropriate or undesirable	
CC	complement activation (e.g. xenograft rejection), inflammatory	
CC	disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),	
CC	post-ischaemic reperfusion conditions, infection or sepsis,	
CC	immune complex disorders and autoimmune diseases (e.g. rheumatoid	
CC	arthritis), proliferative nephritis and myasthenia gravis), and	
CC	reproductive disorders.	
XX		
SQ	Sequence 591 BP; 127 A; 159 C; 151 G; 154 T; 0 other;	
Query Match	97.8%; Score 578.2; DB 19; Length 591;	
Best Local Similarity	98.6%; Pred. No. 2.5e-186;	
Matches 583; Conservative	0; Mismatches 8; Indels 0; Gaps	0;
QY	1 ATGCAGTCACACGCTCCGGATGSGCTGCGGCGCCGACCAACCTGACTATGAA	60
DB	1 atgcagtgaacacgcctcggaaatgctgcgttcgcgcgcgcgaaccaactgactatgaa	60
QY	TTTGAGTTCGCCGATGGGACCTACTGAACTACGAATGCCGCCGGGTATAGCGCGCC	120
DB	61 tttagattcccgatgcgtgaactactgaactgaactgaatgctgcgcgcgttatagcgcgccg	120
QY	CCGTTTTCATCATCTGCGCTGAAACACTCTGCTGAGACTGCTGAAGACCGGTGCCGA	180
DB	121 ccgttttcatcatctgcttgcctgtaaaaactctgcctggaactgctgtaaaacccgttcgcga	180
QY	CGTAAATCTGTGTAATCCGCAGATCCGGTTAACGGCAGTGGATGATGATCAAGGC	240
DB	181 cgtaaatctgtgtcgttaatccgcagatccggttaaacggcagtgatgattgattcaaggc	240
QY	ATCCAGTTCGGTTCCTCAATTAATATCTTGTACTAAGGTTACCGTGTGATTGGTTC	300
DB	241 atccagttccggttcctccaattaaatacttctgactaaaggttaccgttgcattgcttc	300
QY	TCCAGCGCTACATGCATATCTCTGGTGATGTCATTTGGGATTAAGAACAGCAGATT	360
DB	301 tccagcgctacatgcatatctctctggtgtaactgctcatattgggaataatgaacacccgatt	360
QY	TGTGACGGAATTCGCTGTGGTCTGCCGCCGACCATCGCCACAGGATGATTTCACCTCTATC	420

Db		361	ttgtaccgaatctcgtgtgtcttcgccgcgcacatcgcgaacggttgatttcaacctatc	420
Oy		421	AGTCCGACGATTTTTCATATGATGTTCTGTGGACGATACCACTGCATATCTGGTAGCGGT	480
Db		421	atgtcgcgagatttccatacgtttctgtgtgtgacacacgttccaatccggtgagcgt	480
Oy		481	GGTAAAAAGGTGTTGAGCTGTGGGTAGAGCCGTCATCTACTGACACTAGCAAGAAGCAT	540
Db		481	gtctgtaagtggtttgagctcgtgtgtgtagcgcgtccatctatctgacacagtaagcagat	540
Oy		541	CAAGTGGGCACTCTGGAGCGGCCCGCACCGACATGTCATCATCCGAGACAA	591
Db		541	caagtggtgcatcttgagcgcgcgcgcacgcagtgatcatccgcgaacaa	591
RESULT	6			
ID	V53271	standard; DNA; 591 BP.		
XX	V53271;			
XX	18-JAN-1999	(first entry)		
DE		Complement receptor type 1-like sequence CM3 DNA.		
XX				
KW		Complement receptor type-1; CRI; CM3; complement; inhibitor;		
KW		anti-thromolytic; multiple sclerosis; Parkinson's disease;		
KW		xenograft rejection; inflammation; Crohn's disease; asthma;		
KW		pneumocystis; post-ischaemic reperfusion; infection; sepsis;		
KW		autoimmune disease; rheumatoid arthritis; proliferative nephritis;		
KW		myasthenia gravis; reproductive disorder; therapy; ss.		
XX				
OS		Homo sapiens.		
OS		Synthetic.		
PN		W09839433-A1.		
PD		11-SEP-1998.		
PF		05-MAR-1998; 98WO-GB00727.		
PR		05-MAR-1997; 97GB-0004519.		
PA		(ADPR-) ADPROTECH PLC.		
PI		Cox VF, Mossakowska DEI, Smith RAG;		
DR		WPI; 1998-506358/43.		
DR		P-PSDB; W79239.		
XX				
PT		Soluble polypeptide comprising short consensus repeats from LHR-A -		
PT		used to treat disorders and diseases associated with inflammation or		
PT		inappropriate complement activation		
PS		Claim 22; Page 46; 67pp; English.		
XX				
CC		This DNA sequence encodes CM2 (see W79239), a protein that consists		
CC		of the short consensus repeats (SCR) 1 and 2 from complement		
CC		receptor type 1 (CRI) fused to an SCR3 (see W79244) in which 1 amino		
CC		acid was altered to that found in the SCR3 of the CRI-1-like		
CC		pseudogene (Cripse) putative product. CM3 DNA was constructed by		
CC		site-directed mutagenesis (see V53265) of plasmid pDB1013-5, which		
CC		codes for SCR1-3 of CRI. pProcSCR1-3CM3 carrying CM3 DNA was used		
CC		to transform Escherichia coli BL21(DE3), and CM3 was purified from		
CC		solubilised inclusion bodies. The invention provides DNA sequences		
CC		(see V53262 and V53269-79) encoding novel soluble engineered CRI		
CC		polypeptides (see W53236-47) such as CM3 that act as complement		
CC		inhibitors with functional complement inhibitory including		
CC		anti-thromolytic activity. These can be used to treat a disease or		
CC		disorder associated with inflammation or inappropriate complement		
CC		activation, such as neurological disorders (e.g. multiple sclerosis		
CC		and Parkinson's disease), disorders of inappropriate or undesirable		



```

Db 571 agagagattttcactatgatcagtgtagaccacgcgtgcaatcctggaagcggagg 630
QY 484 AAAAAGTGTGAGCTCGTGGGTGAGCCGTCATCTACTGACTAGCAAGAGATCAA 543
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 631 agaaagtgcttgagcttggtgtagagccctcatalactgacacagcaatgacgtcaa 690
QY 544 GTGGGCACTTGAGAGCGGCGCCGACCGCATGTCATCCCGAACA 591
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 691 gtgggcatctgagcggcccgccctcactgaltactaactaaca 738

RESULT 8
Q11642
ID Q11642 standard; DNA; 6951 BP.
AC Q11642;
XX
XX 25-JUN-1991 (first entry)
DT
XX
DE Entire human complement type 1 receptor coding region.
KW complement system; C3b/C4b receptor; CRI; allergic reaction;
KM Immune response; clone lambda T109.1; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 28..147
FT /tag= a
FT /note= "putative"
FT mat_peptide 148..6144
FT /tag= b
FT /product= C3b/C4b receptor

WO9105047-A.
XX
PN 18-APR-1991.
XX
PD
XX
PE 25-SEP-1990; 90MO-US05454.
XX
PR 26-SEP-1989; 89US-0412745.
XX
PR 26-SEP-1990; 90US-0912349.
XX
PA (TCEL-) T CELL SCI INC.
PA (UYJO ) JOHNS HOPKINS UNIVERSITY.
PA (BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
XX
PI Fearon DT, Klickstein LB, Wong WW, Carson GR, Hoh M, Conclino MF;
PI Makrides SC, Marsh HC;
XX
XX WPI, 1991-132854/18.
DR P-PSDB; R11810.
XX
XX Human complement receptor type 1 gene, encoded proteins and
PT fragments - for treatment of immune disorders; myocardial infarct,
PT damage due to inflammation and in treatment of thrombosis
XX
XX Claim 1; Fig 1; 234pp; English.
XX
XX This sequence is a composite of sequences isolated as lambda clones
CC H10.3, T109.1, H3.1 and H7.1. The clones were present in the
CC specifically primed lambda g11 cDNA library (Lambda HH) which was
CC prepared with cDNA synthesised from poly(A)+ RNA from DMSO induced
CC HL-60 cells. The library was screened using probes CRI-1, CR-2 and
CC CRI-4 (see Wong, WW et al., 1985, Proc. Nat. Acad. Sci. USA, 82:7711)
CC and probe CRI-18 (corresponding to nucleotides 101-352 of this
CC sequence). There are four direct, long homologous repeats of 450bp,
CC each comprising 7 short consensus repeats. Nucleotides 28-1533 are
CC also claimed separately.
CC See also Q11643.
XX
XX Sequence 6951 BP; 1802 A; 1681 C; 1659 G; 1809 T; 0 other:
SO

```

```

Query Match 75.7%; Score 447.2; DB 12; Length 6951;
Best Local Similarity 85.0%; Pred. No. 2,4e-141;
Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 4 CAGTGCACACCTCCGGAAATGGCTGCCGTTCGCCGCCGACCAACGATGATGATTT 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 151 caatgcaatgccccagaatgcttccatctgcagagctcaactcaactgatatgtt 210
QY 64 GAGTCCCGATCGGATCTACTGAACTAGCAATGCGCGGCTTATGACGCCGCCG 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 211 gatttcccaatggaatactcgaataatgaaatgcccctggttctccgaagaacgg 270
QY 124 TTTTCTATCATCTGCTCGTGAAGAACTCTGTGTGAGCTGTGCTAAGACCGTTGCCAGT 183
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 271 ttctctatcatctgcctaaactcagctctgagcgtgctgaagcaggtgcagagcgt 330
QY 184 AATCTGTGTGTAATCCGCCAGATCCGCTTAACGGCATGTCATGATCAAGCATC 243
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 331 aaatcagtgctgaatccctcagatcctgtaatgcatggtgcatgataaaggatc 390
QY 244 CAGTTCGATCCCAATTAATATCTTGTACTAAGATACCGTGTGATGTTCTCTCC 303
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 391 cagttcgagatcccaataataatctctgtacataaagaatacagactcattgtctcg 450
QY 304 AGCGCTACATGATCATCTGTGTGATGATGTCATTTGGATAATGAACCGATTGT 363
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 451 tctgcacatgcatcactcagtgatcatctgctattggtatgataaaccatttctg 510
QY 364 GACCGAATTCGGTGTGTGTCGCCGCCGACCATGCGCAACGATGATTCACCTCATAGT 423
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 511 gaagaatcccttggtggctaccccccaatacaatgaatgattcattagaccac 570
QY 424 CGCGAGTATTTTACATGATGTTCTGTGTGACCTACCATGTCATCTGAGTACCGCTG 483
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 571 agagagattttcactatgatcagtgtagaccacgcgtgcaatcctggaagcggagg 630
QY 484 AAAAAGTGTGAGCTCGTGGGTGAGCCGTCATCTACTGACTAGCAAGAGATCAA 543
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 631 agaaagtgcttgagcttggtgtagagccctcatalactgacacagcaatgacgtcaa 690
QY 544 GTGGGCACTTGAGAGCGGCGCCGACCGCATGTCATCCCGAACA 591
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 691 gtgggcatctgagcggcccgccctcactgaltactaactaaca 738

RESULT 9
ID Q11642 standard; DNA; 6951 BP.
XX
XX 238150;
AC 238150;
XX
XX 22-FEB-2000 (first entry)
DT
XX
DE Human C3b/C4b receptor (CRI) protein encoding DNA.
XX
XX C3b/C4b receptor; CRI protein; cell-surface protein; erythrocyte; human;
KW complement regulatory activity; complement pathway enzyme; tissue damage;
KW reperfusion injury; Arthus reaction; myocardial infarct; inflammation;
KW heart condition; autoimmune disorder; diagnostic; ss.
XX
XX Homo sapiens.
XX
XX US5981481-A.
XX
XX 09-NOV-1999.
PD
XX
XX 06-JUN-1995; 95US-0470652.
PF
XX
XX 03-APR-1989; 89US-0332865.
PR 06-DEC-1974; 74US-0350238.
PR 24-FEB-1993; 93US-0026134.

```





is found in plasma which has ligand binding activity and the same molecular weight as membrane-associated CRI. CRI binds C3b and C4b that have covalently attached to immune complexes and other complement activators. The consequences of these interactions depends on the type of bearing the receptor. Erythrocyte CRI binds immune complexes for transport to the liver. CRI on neutrophils and monocytes internalises bound complexes, either by adsorptive endocytosis or by phagocytosis. The function of CRI on B lymphocytes is less well defined. CRI can inhibit the classical and alternative pathway C3/C5 convertases and act as a cofactor for the cleavage of C3b and C4b by factor I, therefore CRI has a complement regulatory function as well as acting as a receptor. CRI is a glycoprotein composed of a single polypeptide chain. Four allelotypic forms of CRI have been identified, differing by increments of approx 40-50 kD. The two most common forms, the F and S allotypes, also termed A and B allotypes, have molecular weights of 250 and 290 kD respectively. The two rarer forms have molecular weights of 210 and 290 kD. These differences represent differences in the polypeptide chain of CRI, rather than glycosylation state because they are not abolished by treatment of purified receptor protein with endoglycosidase F. The CRI gene has been shown to have repetitive intervening sequences which may have been duplicated in the formation of the larger allotypes.

SQ Sequence 6951 BP; 1799 A; 1692 C; 1648 G; 1807 T; 5 other;

Query Match	75.0%	Score 443.2	DB 14	Length 6951
Best Local Similarity	84.4%	Pred.No.5.4e-140		
Matches 496; Conservative	0	Mismatches 92	Indels 0	Gaps 0

QY	4	CAGTGGCAACGGTCCGGAAATGGCTCCCGTTCGCGCGCCGACCAACCGTACGATGAATTT	63
Db	151	caatgcaatgcccagaatggtcttccatttgcagcgcttaccacccaactacgaagagtc	210
QY	64	GAGTCCCGATCGGTACCTACCTAGCATACGAATGCCGCCGGGTATAGCGGCCCGC	123
Db	211	gagttcccatcttggaacatctcgaactaagatgacgcgccttgatttccgaaagacg	270
QY	124	TTTTCTATCATCTGCGCTGAAAACCTGTGTCTGACCTGGTGTAAAGACCGTTGCCAGCT	183
Db	271	ttctctacatctcgtctaaaaaacctcagctctgacatggtgctaaagacaggtgcacgct	330
QY	184	AAATCTTCTCTAATCCGCCAGATCCGGTTTAAGGCAATGGGCAATGATCAACAAAGCATC	243
Db	331	aaatcaatgctgaatccctccagaatcccgtagaaggaaggaagctgatacaaaagacatc	390
QY	244	CAGTTCCGTTCCCAATTAATTAATTTCTGTATCTAAAGTTACCTCGATGTGTTCTCTCC	303
Db	391	cagttcggaatcccaaatataatcttctgtactaaagataacgacccatttgttctctcg	450
QY	304	AGCCCTACATCATCATCTCTGTGTGATCTGTCAATTTGGATAATGAACACCGATTTGT	363
Db	451	tctgcacaatgcacatcatctcagctgatactgctcatcttggaataagaaacacattttn	510
QY	364	GACCGAATTCGGTGTGTCGCCGCCGACCACTCCGCAACGATGATTTCACCTATATAGT	423
Db	511	mncgaatctcttcttgggttctaccccccaaccacccaactgaatgattctatagacaac	570
QY	424	CGCGAGTATTTTCACTATGATTGTGTGGTGACACACACTGCATCTGGGAGCGGTGT	483
Db	571	agtagaattcttcaactaagataagtaagtgtagccttaacgcgttcgaaatccttgaaagtcgagcg	633
QY	484	AAAAAGTGTTTGAGCTGTGGGTGAGGCGGTGCATCTACTGCACATAGCAAAAGATCAAA	543
Db	631	agaaagtgcttgagccttggtggtgagccctccatatagtcaccacgacaatgacatcaa	690
QY	544	GTGGCATCTGGAGCGCGCCCGGCAACGAGTGCATCAATCCGAACAA	591
Db	691	gttgggcatctvgaaagtcgcccgcctctaagtgacattacctaaca	738

RESULT 11  
Q11643

ID		Q11643 standard; cDNA; 5420 BP.
XX		
AC		Q11643;
XX		
DT		25-JUN-1991 (first entry)
XX		
DE		Partial human complement type 1 receptor coding region.
XX		
KM		complement system; C3b/C4b receptor; CRI; allergic reaction;
KW		immune response; ss.
XX		
OS		Homo sapiens.
XX		
FH		Key location/Qualifiers
FT		3..4614
FT	CDS	/*tag= a
FT		/product= CRI
PN		WO9105047-A.
XX		
PD		18-APR-1991.
XX		
PE		25-SEP-1990; 90WO-US05454.
XX		
PR		26-SEP-1989; 89US-0412745.
PR		26-SEP-1990; 90US-0912349.
XX		
PA		(TCEL-) T CELL SCI INC.
PA		(UJJO) JOHNS HOPKINS UNIVERSITY.
PA		(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
XX		
PI		Fearon DT, Klicstein LB, Wong WW, Carson GR, Hoh M, Concino MF,
PI		Makrides SC, Marsh HC;
DR		WP1: 1991-132854/18.
DR		P-PSDB; R11982.
XX		
PT		Human complement receptor type 1 gene, encoded proteins and
FR		fragments - for treatment of immune disorders, myocardial infarct,
PT		damage due to inflammation and in treatment of thrombosis
XX		
PS		Claim 1; Fig 1; 234pp; English.
XX		
CC		Ten overlapping cDNA clones spanning 5.5kb were isolated from a
CC		tonsillar library and sequenced in whole or in part. A single long
CC		ORF beginning at the 5' end of the clones and extending 4.7kb
CC		downstream to a stop codon was identified. This sequence represents
CC		about 80 per cent of the estimated 6kb of coding sequence for the F
CC		allotype of CRI. It contains 3 tandem, direct, long homologous
CC		repeats; the full-length gene encodes 4 LHR's.
CC		See also Q11642.
XX		
SQ		Sequence 5420 BP; 1435 A; 1295 C; 1263 G; 1427 T; 0 other;

Query Match	55.4%; Score 327.2; DB 12; Length 5420;
Best Local Similarity	72.3%; Pred.No. 1.1e-100;
Matches 425; Conservative	0; Mismatches 163; Indels 0; Gaps 0;

OY	4	CAGTGCAACGCTCCGGATGCGTGTTCGCCGGCCGCCGACCACCTGACTGATAATT	63
Db	1320	cactgtcaagcccccgcgatcatcttctgttcgccaagtgtgaanaaccnaacccatgcatc	1379
OY	64	GAGTCCCGCAGCGGNACCTACCTGAACGAAATGCGCCCGGGTTAAGGCGCCGCCG	123
Db	1380	gaattccccatggagacaaccttaagaagcaaaabgcgtcttgactaacggaggcgca	1439
OY	124	TTTTCTATCATCTGCGCTGAAAAAAGTCTGTGAGCTGSGTGTAAAGAACCGTGGACGT	183
Db	1440	ttctctatcacatgctagataaacctgtctggtcgaagtcaccaagaatgctgtataaagt	1499
OY	184	AAATTTGTCTGTAATCCCGCCAGATCCGGTTAAGCGCATGAGTGATCAAGGCATC	243

Query Match	55.48;	Score 327.2;	DB 12;	Length 5420;
Best Local Similarity	72.38;	Pred. No. 1.1e-100;		
Matches 425;	Conservative 0;	Mismatches 163;	Indels 0;	Gaps 0

QY	4	CAGTGCACACGTCCTCCGGAATGGCTGCCCTTGCGCGCGCCGACACCAACCTGATGATGAATTT	63
Db	1320	cactgtcaagcccccagatcatcttctctgttcgcaagttgaaaccccaaccaatgctctc	1370
QY	64	GAGTTCCCGATCCGTTACCTACCTAACTAGGAATGCCGCCCGGTTATTACGGCGCCCG	123
Db	1380	gacttcccatctggacatctttaaagtaagaaatgacgctctgagtactacggaagcgca	1430
QY	124	TTTTCATCATCTCCCGCGAAATACTCTGTCTGACATGTGTCTAAGACCTTGGCACT	183
Db	1440	tctctctacacatctcttagataaaccttgctcttggcacaagttgctcttaaacgct	1490
QY	184	AAATCTTGCTATTCGCCCGACGATCCGGTTAACGGCATGTGATGATCAAAAGCATC	243



KM		autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KM		myasthenia gravis; reproductive disorder; therapy; ss.
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	W09839433-A1.	
PD	11-SEP-1998.	
XX		
PF	05-MAR-1998; 98WO-GB00727.	
XX		
FR	05-MAR-1997; 97GB-0004519.	
XX		
PA	(ADPR-) ADPROTECH PLC.	
XX		
PI	Cox VF, Mossakowska DEL, Smith RAG;	
DR	WPI: 1998-506358/43.	
P-PSDB:	P-PSDB: W79247.	
PT	Soluble polypeptide comprising short consensus repeats from LHR-A -	
PT	used to treat disorders and diseases associated with inflammation or	
PT	inappropriate complement activation	
XX		
XX		
PS	Claim 22; Page 51; 67pp; English.	
XX		
CC	This DNA sequence encodes CM14 (see W79246), a protein that consists	
CC	of the short consensus repeat 3 (SCR3) of the putative product of	
CC	CR1-like pseudogene Crispse. This SCR3 is also found in polypeptide	
CC	CM7 (see W79236). Plasmid pBROSCRI-3CM14 was used to transform	
CC	<i>Escherichia coli</i> BL21(DE3), and CM14 was purified from solubilised	
CC	inclusion bodies. The invention provides DNA sequences (see V53262	
CC	and V53266-79) encoding novel soluble engineered CR1 polypeptides	
CC	(see W53235-47) such as CM14 that act as complement inhibitors with	
CC	functional complement inhibitory, including anti-haemolytic,	
CC	activity. These can be used to treat a disease or disorder	
CC	associated with inflammation or inappropriate complement activation,	
CC	such as neurological disorders (e.g. multiple sclerosis and	
CC	Parkinson's disease), disorders of inappropriate or undesirable	
CC	complement activation (e.g. xenograft rejection), inflammatory	
CC	disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),	
CC	post-ischaemic reperfusion conditions, infection or sepsis,	
CC	immune complex disorders and autoimmune diseases (e.g. rheumatoid	
CC	arthritis, proliferative nephritis and myasthenia gravis), and	
CC	reproductive disorders.	
XX		
SO	Sequence 228 BP; 50 A; 62 C; 62 G; 54 T; 0 other;	
Query Match	38.1%; Score 225; DB 19; Length 228;	
Best Local Similarity	100.0%; Pred. No. 1e-66;	
Matches 225; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	367 CGAATTCGGTGTGCTCGCCGCCGCACCAACGCAACGAGATTTCACCTCATAGTCG	426
Db	4 cgaatccgtgcygcctcgcgcgcacacacgcgaacagcgattcacccctatccgctgc	63
OY	427 GAGTAATTTACTATAGTGTTCTGTGTGACCTACACACTGCAATCTGGGTAGCCGTGTAA	486
Db	64 gagaatttcactaatcagtctctgtgygacctaccactgaaatctggtagccgtgttaa	123
OY	487 AAGGATTTGACCTGCTGGTGAGCCGCTCCATCTACTGACATAGCAAAGAAGCATCAAGC	546
Db	124 aaggatgtttgaagctcgttgtagccgcatcattactgactagcaaaagatccaagt	183
OY	547 GGCATCTGGAGCGCCCGCACCGACGACATCATATCCGAACA 591	
Db	184 ggcatctggagcgccccgcgcacgcagtcattcatctccgaacaaa 228	
RESULT	14	
V53278		

ID	V53278 standard; DNA; 228 BP.
XX	
AC	V53278:
XX	
DT	18-JAN-1999 (first entry)
DE	
XX	Complement receptor type 1-like sequence CM13 DNA.
XX	
KW	Complement receptor type-1; CR1; CM13; complement; inhibitor;
KW	anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW	xenograft rejection; inflammation; Crohn's disease; asthma;
KW	pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW	autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KX	myasthenia gravis; reproductive disorder; therapy; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO9839433-A1.
PD	
PF	11-SEP-1998.
PR	
PR	05-MAR-1998; 98MO-GB00727.
PA	
PA	05-MAR-1997; 97GB-0004519.
XX	(ADPR-) ADPROTECH PLC.
PI	
PI	Cox VF, Mossakowska DEI, Smith RAG:
DR	WPI; 1998-506358/43.
DR	P-PSDB; w79246.
PT	
PT	Soluble polypeptide comprising short consensus repeats from LHR-A -
PT	used to treat disorders and diseases associated with inflammation or
PT	inappropriate complement activation
XX	
XX	Claim 22: Page 51; 67pp: English.
CC	This DNA sequence encodes CM13 (see W79246), a protein that consists
CC	of the short consensus repeat 3 (SCR3) of complement receptor type
CC	1 (CR1) in which 6 amino acid residues have been substituted by
CC	the amino acids theoretically encoded by CR1-like pseudogene
CC	Cripse. This SCR3 is also found in polypeptide CM6 (see W79241).
CC	Plasmid pProSCRI-3CM13 carrying CM13 DNA was used to transform
CC	Escherichia coli BL21(DE3), and CM13 was purified from solubilised
CC	inclusion bodies. The invention provides DNA sequences (see V53262
CC	and V53266-79) encoding novel soluble engineered CRI polypeptides
CC	(see W53266-77) such as CM13 that act as complement inhibitors with
CC	functional complement inhibitory, including anti-haemolytic,
CC	activity. These can be used to treat a disease or disorder
CC	associated with inflammation or inappropriate complement activation,
CC	such as neurological disorders (e.g. multiple sclerosis and
CC	Parkinson's disease), disorders of inappropriate or undesirable
CC	complement activation (e.g. xenograft rejection), inflammatory
CC	disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
CC	post-ischaemic reperfusion conditions, infection or sepsis,
CC	immune complex disorders and autoimmune diseases (e.g. rheumatoid
CC	arthritis), proliferative nephritis and myasthenia gravis), and
CC	reproductive disorders.
XX	
SO	Sequence 228 BP; 53 A; 62 C; 60 G; 53 T; 0 other;
OY	
OY	Query Match 36.7%; Score 217; DB 19; Length 228;
OY	Best Local Similarity 97.8%; Pred. No. 5.4e-64;
OY	Matches 220; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DQ	367 CGAATTCGGTGTGCTCCGCCGCACATCGCAGTGATTCACTCATGACGCGC 426
DQ	
DQ	4 cgaatccgctgtgtcctcgccgcagacataccaacagtgattcatcttcaaccatgc 63
DQ	47 GAGTATTTTCACTATGCTTCTGTGTGGTAGCCTACCACTGCAATCTGGTAGCCGTGTGAAA 486

```

|||||
Db 64 ggaatttcacacatgctgctggtgacctaccacgcatctggtgctgataa 123
QY 487 AAGGTGTTGAGCTGCTGAGCGGTCATCATGCTAGTACGAAAGCATCAAGTG 546
Db 124 aaggtgcttgagctcgtggtgagccgctccatctactgacctgcaaaagcagatcaagt 183
QY 547 GGCATCTGAGAGCGGCCGACCCGACATGCATCATCCGAAACAA 591
Db 184 ggcattctgagcgccgcgcagctgcatccccaacaa 228

```

## RESULT 15

V53277

ID V53277 standard; DNA; 228 BP.

XX V53277;

AC 18-JAN-1999 (first entry)

XX 18-JAN-1999 (first entry)

DE Complement receptor type 1-like sequence CM12 DNA.

XX Complement receptor type-1; CR1; CM12; complement; inhibitor;

KM anti-haemolytic; multiple sclerosis; Parkinson's disease;

KM xenograft rejection; inflammation; Crohn's disease; asthma;

KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;

KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;

KM myasthenia gravis; reproductive disorder; therapy; ss.

XX Homo sapiens.

OS Synthetic.

XX WO9839433-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98MO-GB00727.

XX 05-MAR-1997; 97GB-0004519.

XX (ADPR-) ADPROTECH PLC.

XX Cox VE, Mossakowska DET, Smith RAG;

XX WPI: 1998-506358/43.

XX P-PSDB: W79245.

XX Soluble polypeptide comprising short consensus repeats from LHR-A -

PT used to treat disorders and diseases associated with inflammation or

PT inappropriate complement activation

XX Claim 22: Page 50; 67pp; English.

This DNA sequence encodes CM12 (see W79245), a protein that consists of the short consensus repeat 3 (SCR3) of complement receptor type 1 (CR1) in which 5 amino acid residues have been substituted by the amino acids theoretically encoded by CR1-like pseudogene CR1pse. This SCR3 is also found in polypeptide CM5 (see W79240). Plasmid pProSCRI-3CM12 carrying CM12 DNA was used to transform *Escherichia coli* BL21(DE3), and CM12 was purified from solubilised inclusion bodies. The invention provides DNA sequences (see W53262 and W53269-79) encoding novel soluble engineered CR1 polypeptides (see W53236-47) such as CM12 that act as complement inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or disorder associated with inflammation or inappropriate complement activation, such as neurological disorders (e.g. multiple sclerosis and Parkinson's disease), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection), inflammatory disorders (e.g. Crohn's disease, asthma, and acute pancreatitis), post-ischaemic reperfusion conditions, infection or sepsis, immune complex disorders and autoimmune diseases (e.g. rheumatoid arthritis, proliferative nephritis and myasthenia gravis), and

CC reproductive disorders.

XX Sequence 228 BP; 46 A; 63 C; 65 G; 54 T; 0 other;

SQ

Query Match 36.4%; Score 215.4; DB 19; Length 228;

Best Local Similarity 97.3%; Pred. No. 1.9e-63;

Matches 219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 367 GGAATTCGGTGTGCTGCTGCGCCGACCATCGCCAAAGGTGATTCCTCATAGTCC 426

Db 4 cgaattccgtgtgctgctgcccgcacacatcgcaagtgatctacatcctatactgcg 63

QY 427 GAGATTTTCACTATGAGTCTGTGTGAGACCTACCACTGCATCTGGGTAGCCGTGTA 486

Db 64 ggaatttcactatggtctctgtgtgacctaccgctgcaatccggtagcggtgctcgt 123

QY 487 AAGGTGTTGAGCTGCTGAGCGGTCATCATGCTAGTACGAAAGCATCAAGTG 546

Db 124 aaggtgcttgagctcgtggtgagccgctccatctactgacctgcaaaagcagatcaagt 183

QY 547 GGCATCTGAGAGCGGCCGACCCGACATGCATCATCCGAAACAA 591

Db 184 ggcattctgagcgccgcgcagctgcatccccaacaa 228

Search completed: January 13, 2001, 13:12:07  
 Job time: 2387 sec



**THIS PAGE BLANK (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:30:50 ; Search time 65.7 Seconds  
(without alignments)  
1449.707 Million cell updates/sec

Title: US-09-380-682-2

Sequence: 1 ATGCAGTCGACACGCTCCGGA.....AGTCATCATCCGACACAA 591

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 280836 segs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents,NA:\*

- 1: /cgn2\_6/prodata/2/lna/5A\_COMB.seq:\*
- 2: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:\*
- 4: /cgn2\_6/prodata/2/lna/PCITUS\_COMB.seq:\*
- 5: /cgn2\_6/prodata/2/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558.2	94.5	605	2	US-08-769-967A-33
2	447.2	75.7	6951	5	5256642-1
3	447.2	75.7	6951	5	5472939-1
4	327.2	55.4	5420	5	5256642-3
5	327.2	55.4	5420	5	5472939-3
6	204.2	34.6	243	2	US-08-769-967A-32
7	101.1	17.1	101	2	US-08-356-361-3
8	101.1	17.1	101	2	US-08-356-361-4
9	101.1	17.1	101	2	US-08-356-361-5
10	101.1	17.1	101	2	US-08-356-361-6
11	101.1	17.1	101	2	US-08-769-967A-3
12	101.1	17.1	101	2	US-08-769-967A-4
13	101.1	17.1	101	2	US-08-769-967A-5
14	101.1	17.1	101	2	US-08-769-967A-6
15	93.3	15.7	93	2	US-08-356-361-2
16	93.3	15.7	93	2	US-08-769-967A-2
17	86.4	14.6	94	2	US-08-356-361-7
18	86.4	14.6	94	2	US-08-769-967A-7
19	86.4	14.6	87	2	US-08-356-361-1
20	86.4	14.6	87	2	US-08-769-967A-1
21	78.4	13.3	90	2	US-08-356-361-8
22	78.4	13.3	90	2	US-08-769-967A-8
23	75.4	12.8	85	2	US-08-356-361-11
24	75.4	12.8	85	2	US-08-769-967A-11
25	75.4	12.8	85	2	US-08-769-967A-12
26	75.4	12.8	85	2	US-08-769-967A-13
27	68.8	11.6	79	2	US-08-356-361-13
28	68.8	11.6	79	2	US-08-769-967A-13

c 29	68	11.5	78	2	US-08-356-361-10	Sequence 10, Appl
c 30	68	11.5	78	2	US-08-769-967A-10	Sequence 10, Appl
c 31	61.8	10.5	81	2	US-08-356-361-21	Sequence 21, Appl
c 32	61.8	10.5	81	2	US-08-769-967A-21	Sequence 21, Appl
c 33	60.8	10.3	75	2	US-08-356-361-14	Sequence 14, Appl
c 34	60.8	10.3	75	2	US-08-769-967A-14	Sequence 14, Appl
c 35	60	10.2	72	2	US-08-356-361-9	Sequence 9, Appl
c 36	60	10.2	72	2	US-08-769-967A-9	Sequence 9, Appl
c 37	58.4	9.9	85	2	US-08-356-361-22	Sequence 22, Appl
c 38	58.4	9.9	85	2	US-08-769-967A-22	Sequence 22, Appl
c 39	44.6	7.5	860	1	US-08-310-416A-19	Sequence 19, Appl
c 40	44.6	7.5	860	1	US-08-888-171-19	Sequence 19, Appl
c 41	44.6	7.5	969	1	US-08-310-416A-12	Sequence 12, Appl
c 42	44.6	7.5	969	1	US-08-888-171-12	Sequence 12, Appl
c 43	44.6	7.5	1134	3	US-08-793-418-4	Sequence 4, Appl
c 44	44.6	7.5	1878	2	US-08-435-149-17	Sequence 17, Appl
c 45	44.6	7.5	2096	1	US-08-458-084-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-769-967A-33  
; Sequence 33, Application US/08769967A  
; Patent No. 5859223  
; GENERAL INFORMATION:  
; APPLICANT: Mossakowska, Danuta E.I.  
; APPLICANT: Smith, Richard A.G.  
; APPLICANT: Dodd, Ian  
; APPLICANT: Freeman, Anne Mary  
; TITLE OF INVENTION: Soluble CRI Derivatives  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
; STREET: P.O. Box 1539  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,967A  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/440,569  
; FILING DATE: 15-May-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T.  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: P30423C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 270-5364  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 605 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-769-967A-33  
Query Match 94.5% Score 558.2; DB 2; Length 605;  
Best Local Similarity 97.6% Pred. No. 1.8e-178;  
Matches 577; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

RESULT 2  
 5256642-1  
 Patent No. 5256642  
 APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
 WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F., JR., STEPHEN  
 H.; MAKRIDES, SAVVAS; MARSH, HENRY C., JR.  
 TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
 RECEPTOR 1 (CRL) AND A THROMBOTIC AGENT, AND THE METHODS OF  
 USE THEREOF  
 NUMBER OF SEQUENCES: 30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/588,128  
 FILING DATE: 24-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 412,745  
 FILING DATE: 26-SEP-1989  
 APPLICATION NUMBER: 332,865  
 FILING DATE: 03-APR-1989  
 APPLICATION NUMBER: 176,532  
 FILING DATE: 01-APR-1988  
 SEQ ID NO:1:  
 LENGTH: 6951  
 5256642-1

QY	64	GAGTCCGCAATCGGTACCTAAGCTGAACTACGAAATCCGCCCGGGTTATAGCGCCGCCG	122
Db	211	gaattcccaattcggacacatctgacactgactgatatgcgccttggtttatccggaagcgcg	270
QY	124	TTTTTCATCATCTGCTCGTGA AAAACTGTGCTGGATCGTGTGTAGAGACCGTTGCCAGCT	183
Db	271	ttttcctacatctgccttaaaaaaccagttcgtgactggtgtcctaaagacagtgtagagcgt	330
QY	184	AAATCTATGCGTAATCCGCCAATCCGGTTAACGGCATGTGCATGTGATGACCAAGGCATC	243
Db	331	aattctctgcgaaactccctccagatctctgtaactgtaatgcatgcatgcatgaagcattc	390
QY	244	CAGTTGGTTCCCAATTAATATATCTGTACTGAAGTTAACGTCATGATGTTGTTCTCTCC	303
Db	391	cagttcgatcccaataataattctgtctcctaaagaaacagacccattggttctctcg	450
QY	304	AGGCGTACATGGATATATCTCTGGTGAATCTGTCTCATTTTGGATATGAAACCCGATTTGT	363
Db	451	tctgcacatgatatcatctcagtgatcactgctatttggtatataagaaacctatttgc	510
QY	364	GACCGAATTCGGTGTGTGCTGCCGCCACCATCGGCCAACGCTGATTTACACTCTATCACT	423
Db	511	gacaaatctctctgtyggctacccccaccatcaaccatgaggaattcttcagcccaac	570
QY	424	CGCGAGTATTTTCACTAATAGTGTCTGCTGCTGATCACTACCATCGCAATCGGTGGCCGTGT	483
Db	571	agagagaatttctcctactgatacgaagtgatgtaacctacacgtctgcaatctctggaagcggagcg	630
QY	484	AAAAAGGTGTTAGCTCGTGGGTGAACCCCTCCATCTACTGCACATGCAAAAGCATATA	543
Db	631	agaaagaggttcgtgactctgtyggtagccctccatatctactgacacagcaatgacgatcaa	690
QY	544	GTGGGCACTGTGAACGCCGCCGACCGCAACGGATGATATCCCAACAAA	591
Db	691	gtgggcatctcgagcggcccgccctccctcagtgcatataatccctaaacaaa	738



Db	211	gagttcccatlvggacatctcigaactaigaatgcccgccttgtatcttcgcgaagacg	270
Qy	124	TTTTTATCATCTGCGTGAATAAAGCTGTGTCTGGACTGTGTGCTAAAGACCGTCCGACGT	183
Db	271	ttttatcatctcgtcctaaanaactcagtcctgacctgtgtctaagacagctgcagacgt	330
Qy	184	AAATCTTGCTATTCGCCGACATCCGGTTAACGGCATGGTGCATGTGATCAAAAGGCATC	243
Db	331	aaatcatctcgtatctcccccagatccctgtgaatgcatgtgtgcactgtgataaaggacatc	390
Qy	244	CAGTTCGGTTCACAAATTAATATTCTTGTTGTTACTTAAAGTTAACGGTGTGATGGTGTCTCC	303
Db	391	cagttcgtgatacccaataataatcttctgtactctaagataaccgactcatgtgttctctcg	450
Qy	304	AGCGTTACATGCATCATCTCTGTGTGATACTGTGTCATTTTGGATATGAAACACCGATTTGT	363
Db	451	ctctgcacatgcatacatcctcagtgatgactgtcatcttggataatgaaacactattgt	510
Qy	354	GACGGAATTCGGTGTGTCTGCCGCCGACCATGCCCAACGGTGATTTTACACTTATCAAGT	423
Db	511	gacgaatactcttcttlyggctacccccacatacctcaatgagatattcatatgaaccacac	570
Qy	424	CGCGATGTTTTCATAATGAGTTCGTGTGTGTGACACACATGCAGATCGGTAGACCGGTGG	483
Db	571	agagagaattcttcaactatgatacagctgtgtgacctaccgcctgcacatctctgaaagcgttagg	630
Qy	484	AAAAAGGTGTTGAGCTCTGTGGGTGAGCCGTCATCTTACTTACATGCACATAGACAGCATCA	543
Db	631	agaaagtgctttagactgtgtgtgtagccctccatactacatgcacacagcaatgacgtacaa	690
Qy	544	GTGGGCATCTGAGAGGGGGCCGGACCCGAGATGATCATATCCGCAACAA	591
Db	691	gttgggcatactvgagcgcgcgcctccacagtgatgtattactacttaacaa	738

RESULT 4  
5256642-3  
Patent No. 5256642  
APPLICANT: FERRON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.  
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
RECEPTOR 1 (CRL) AND A THROMBOLYTIC AGENT, AND THE METHODS OF  
USE THEREOF  
NUMBER OF SEQUENCES: 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/0588,128  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 412,745  
FILING DATE: 26-SEP-1989  
APPLICATION NUMBER: 332,865  
FILING DATE: 03-APR-1989  
APPLICATION NUMBER: 176,532  
FILING DATE: 01-APR-1988  
SEQ ID NO.: 3  
LENGTH: 5420  
5256642-3

Query Match	55.4%;	Score 327.2;	DB 5;	Length 5420;
Best Local Similarity	72.3%;	Pred. No. 3.2e-100;		
Matches 425;	Conservative	0;	Mismatches 163;	Indels 0;
			Gaps	0

Accession	Sequence	Length
QY 4	CAGGCAACGGTCCGGATAGGCGCCGCTTGCGCGCCGACACCACTGACTGATGTAATTT	63
Dd 1320	cacgtgaagccaccagttcatlttttgtttgcgaatgtgaacccaaccatgatcact	1379
QY 64	GAGTTCGCCGATCGGTACTACTGTAACGTAAGATGCCGCCGGGTATTATGCGGCCGCCG	123
Dd 1380	gacttcccatcttgacacatctttaaagtaagaatgcgctctcttgatgacacagggagsgca	1439

Oy	124	TTTCTTAAATTCGCGCGAAGAACTCGTGTGACGTGCGTGAAGACCTTCCGACGT	183
Db	1440	ttctctatcaaatgctcagaataactctgtcttgctcaagtcctcaagaatgctctgaacgt	1499
Oy	184	AAATCTGTGTAAATCCCGCAGATCCGGTTAAAGCGATGTGCATGTGATCAAGGATC	243
Db	1500	aatcatgtaaaactctctccagatccagatcgaaatgagatgtagtgcattgtagtcacgaactc	1559
Oy	244	CAGTTCCGTTCCCAAATTAATATTTCTTGTAATAAGGTTACCGTCTGATTGGTTCCGC	303
Db	1560	caggttgatctcagaataccaactatctctgtactacagggaccggaactcatlgtactacca	1619
Oy	304	AGCCGTATCATCATCATCTGTGGTATACGTATTTGGATTAAGAAACACCGATTGT	363
Db	1620	tcctctgaatgtagtacctctcaagcaataacttcccatcttgtagaagcaagccgcaacttgc	1679
Oy	364	GACCGAATTCGGTGTGGTGTGCCGCCGACCATGCCCAAGGATTTCACTCTATCAGT	423
Db	1680	caaggaattccctctgtgggtctaccctcccaacatctgcgaatggattcttaagcaccac	1739
Oy	424	CGCAGATTTTACATATGGTTCTGTGSGAGCTTACCATGTGAATCTGGGTAGCGGTGT	483
Db	1740	agaaagaaatttccactatgtaacaaagtggaactaacgcttgaaattctggaagcagaagg	1799
Oy	484	AAAAAGTGTGGAGCTGTGGGTGAGCGGTCCATCTACTGTGACTGCAAAAGCATATA	543
Db	1800	agaaagtglttgagctgtgtgggtggagccctccataactgtaaccaagcaatgagactaa	1855
Oy	544	GTTGGCATCTGAGACGGGCCCGCAGCCGAGATGATATCCGAAACAA	591
Db	1860	gttggaatcttgagcgggtcccgccctcagttgagattatactctcaaaa	1907

```

RESULT 5
5472939-3
Patent No. 5472939
APPLICANT: EARON, DOUGLAS T.; KICKSTEIN, LLOYD B.;
WINNIE W.; CARSON, GERRAD R.; CONCINO, MICHAEL F.; IP, S.
H.; MAKRIDES, SAVVAS; MASH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDiated DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:3:
LENGTH: 5420
5472939-3

```

Query Match	55.48;	Score 327.2;	DB 5;	Length 5420;
Best Local Similarity	72.38;	Pred. No. 3.2e-100;		
Matches 425;	Conservative	0;	Mismatches 163;	Indels 0;

Accession	Sequence	Position
QY	4 CAGTGCACACGCTCCGGAAATGGCTGACCGCTTCGCGCCGCCACCAACCTGATCATTAATTT	63
Db	1320 caatgtaagaccacagtcacttttcggtttgcgaatgtgaataaccacaaccatgacatct	1379
QY	64 GAGTTCOCGATCGGTACCTACTGAACTACGAATGCCGCCGGTTATACGCGGCCGCCG	123
Db	1380 gacttcccatctggacactctttaagtcacgaatgcgcctcgtactacgaagggagcgca	1439
QY	124 TTTTCTATCATCTGCCGAAAAACTCTGCTGTGACCTGGTGTCTAAGGACCGCTTGCCGACGT	183



```

1  APPLICANT: Dodd, Ian
2  APPLICANT: Freeman Mary A.
3  APPLICANT: Mossakowska, Danuta E.I.
4  TITLE OF INVENTION: No. 5833989el Compounds
5  NUMBER OF SEQUENCES: 31
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Smithline Beecham-Corporate Intellectual Property
8  STREET: P.O. Box 1539
9  CITY: King of Prussia
10 STATE: Pennsylvania
11 COUNTRY: USA
12 ZIP: 19406
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentln Release #1.0, Version #1.25
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/356,361
22 FILING DATE: 03-Jul-1995
23 CLASSIFICATION: 435
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Jervls, Herbert H.
27 REGISTRATION NUMBER: 31,171
28 REFERENCE/DOCKET NUMBER: P30423
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (610) 270-5019
31 TELEFAX: (610) 270-5090
32
33 INFORMATION FOR SEQ ID NO: 5:
34
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 101 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: DNA
41
42 US-08-356-361-5
43
44
45 Query Match 17.1%; Score 101; DB 2; Length 101;
46 Best Local Similarity 100.0%; Pred. No. 6.2e-25;
47 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
48
49 QY 188 CTGTCGTAATCCGCGACATCCGGTTAAACGGCATGTGCATGTGATCAAGGCATCCACT 247
50 Db 1 CTGTCGTAATCCGCGACATCCGGTTAAACGGCATGTGCATGTGATCAAGGCATCCACT 60
51
52 OY 248 TCGGTTCCCAATTAATATCTTGTACTATAAGGTTACCGT 288
53 Db 61 TCGGTTCCCAATTAATATCTTGTACTATAAGGTTACCGT 101
54
55 RESULT 10
56 US-08-356-361-6/c
57 Sequence 6, Application US/08356361
58 Patent No. 5833989
59
60 GENERAL INFORMATION:
61 APPLICANT: Smith, Richard A.G.
62 APPLICANT: Dodd, Ian
63 APPLICANT: Freeman Mary A.
64 APPLICANT: Mossakowska, Danuta E.I.
65 TITLE OF INVENTION: No. 5833989el Compounds
66 NUMBER OF SEQUENCES: 31
67
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: Smithline Beecham-Corporate Intellectual Property
70 STREET: P.O. Box 1539
71 CITY: King of Prussia
72 STATE: Pennsylvania
73 COUNTRY: USA
74 ZIP: 19406
75
76 COMPUTER READABLE FORM:
77 MEDIUM TYPE: Floppy disk
78 COMPUTER: IBM PC compatible
79 OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,361  
FILING DATE: 03-Jul-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jervis, Herbert H.  
REGISTRATION NUMBER: 31,171  
REFERENCE/DOCKET NUMBER: P30423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5019  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-356-361-6

Query Match 17.1%; Score 101; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.2e-25;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 AATCGGCGAGTCCGGTTACGGCATGTGATCAAGAGCATCGATTGGTTC 285  
DB 101 AATCGGCGAGTCCGGTTACGGCATGTGATCAAGAGCATCGATTGGTTC 42  
QY 256 CAATTAAATTTCTTACTAAGGTACCGTCTGATTGG 296  
DB 41 CAATTAAATTTCTTACTAAGGTACCGTCTGATTGG 1

RESULT 11  
US-08-769-967A-3  
Sequence 3, Application US/08769967A  
Patent No. 5859223  
GENERAL INFORMATION:  
APPLICANT: Mossakowska, Danuta E.I.  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman, Anne Mary  
TITLE OF INVENTION: Soluble CRI Derivatives  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,967A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/440,569  
FILING DATE: 15-May-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P30423C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5364  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-769-967A-3

Query Match 17.1%; Score 101; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.2e-25;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GAATCGAATCCCGGGGTATACGGCCCGCGTTTCTATCATCTCGTAATAA 146  
DB 1 GAATCGAATCCCGGGGTATACGGCCCGCGTTTCTATCATCTCGTAATAA 60  
QY 147 CTCTGTGACTGTGCTAAGACCGTTGCCGACGTAAAT 187  
DB 61 CTCTGTGACTGTGCTAAGACCGTTGCCGACGTAAAT 101

RESULT 12  
US-08-769-967A-4/C  
Sequence 4, Application US/08769967A  
Patent No. 5859223

GENERAL INFORMATION:  
APPLICANT: Mossakowska, Danuta E.I.  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman, Anne Mary  
TITLE OF INVENTION: Soluble CRI Derivatives  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,967A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/440,569  
FILING DATE: 15-May-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P30423C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5364  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-769-967A-4

Query Match 17.1%; Score 101; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.2e-25;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 AATGCCCGCCGGGTATAGCGCGCCGTTTCTATCATCTGCTGAAAAAGCTCTGCT 154  
DB 101 AATGCCCGCCGGGTATAGCGCGCCGTTTCTATCATCTGCTGAAAAAGCTCTGCT 42  
QY 155 GAACGTGCTGAAGAGACCGTTCGCGACGTAACTGTCGT 195  
DB 41 GACGTGCTGAAGAGACCGTTCGCGACGTAACTGTCGT 1

## RESULT 13

US-08-769-967A-5  
; Sequence 5, Application US/08769967A  
; Patent No. 5859223

## GENERAL INFORMATION:

APPLICANT: Mossakowska, Danuta E.I.  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman, Anne Mary  
TITLE OF INVENTION: Soluble CRI Derivatives  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,967A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/440,569  
FILING DATE: 15-May-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P30423C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5364  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-769-967A-5

US-08-769-967A-5

Query Match 17.1%; Score 101; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6,2e-25;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 CTGTGCTATCCGCCGATCCGGTTAAGCGCATGTCATGTGATCAAGGATCCAGT 247  
DB 1 CTGTGCTATCCGCCGATCCGGTTAAGCGCATGTCATGTGATCAAGGATCCAGT 60

QY 248 TCGGTCCCAATTAATATCTGTACTAAAGGTACCGT 288  
DB 61 TCGGTCCCAATTAATATCTGTACTAAAGGTACCGT 101

## RESULT 14

US-08-769-967A-6/c  
; Sequence 6, Application US/08769967A  
; Patent No. 5859223

## GENERAL INFORMATION:

APPLICANT: Mossakowska, Danuta E.I.  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman, Anne Mary  
TITLE OF INVENTION: Soluble CRI Derivatives  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,967A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/440,569  
FILING DATE: 15-May-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P30423C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5364  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-769-967A-6

US-08-769-967A-6

Query Match 17.1%; Score 101; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6,2e-25;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 AATCCGCCAGATCCGGTTAAGCGCATGTCATGTATCAAAAGCATCCAGTCC 255  
DB 101 AATCCGCCAGATCCGGTTAAGCGCATGTCATGTATCAAAAGCATCCAGTCC 42

QY 256 CAAATTAATATCTGTACTAAAGGTACCGTGTG 296  
DB 41 CAAATTAATATCTGTACTAAAGGTACCGTGTG 1

## RESULT 15

US-08-356-361-2/c  
; Sequence 2, Application US/08356361  
; Patent No. 5839898

## GENERAL INFORMATION:

APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman Mary A.  
APPLICANT: Mossakowska, Danuta E.I.  
TITLE OF INVENTION: No. 5839898 Compounds  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham-Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA

ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,361  
FILING DATE: 03-Jul-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jervils, Herbert H.  
REGISTRATION NUMBER: 31,171  
REFERENCE/DOCKET NUMBER: P30423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5019  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-356-361-2

Query Match 15.7%; Score 93; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.9e-22;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 TGCAGTGCACGCTCCGATGCTGCGCTGCGCGCCCGGACCAACTGACTGATGAAT 61  
Db 93 TGCAGTGCACGCTCCGATGCTGCGCTGCGCGCCCGGACCAACTGACTGATGAAT 61  
OY 62 TTGAGTCCCGATCGGTACTACTGAACTACG 94  
Db 33 TTGAGTCCCGATCGGTACTACTGAACTACG 1

Search completed: January 13, 2001, 13:10:27  
Job time: 2377 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:28:05 ; Search time 1135.8 Seconds  
(without alignments)  
2662.960 Million cell updates/sec

Title: US-09-380-682-2  
Perfect score: 591  
Sequence: 1 ATGCAGTGCACACGCTCCGGA.....AGTGCATCATCCGACACAAA 591

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues  
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_com: \*  
4: gb\_ov: \*  
5: gb\_ph: \*  
6: gb\_pl1: \*  
7: gb\_pl2: \*  
8: gb\_pr1: \*  
9: gb\_pr2: \*  
10: gb\_pr3: \*  
11: gb\_ro: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: em\_fun: \*  
15: em\_hum1: \*  
16: em\_hum2: \*  
17: em\_in: \*  
18: em\_com: \*  
19: em\_ov: \*  
20: em\_ov: \*  
21: em\_pat: \*  
22: em\_ph: \*  
23: em\_pl: \*  
24: em\_ro: \*  
25: em\_sts: \*  
26: em\_sy: \*  
27: em\_un: \*  
28: em\_vl: \*  
29: gb\_ba3: \*  
30: gb\_in1: \*  
31: gb\_in2: \*  
32: gb\_in3: \*  
33: gb\_pr4: \*  
34: gb\_pr4: \*  
35: em\_ba1: \*  
36: em\_ba2: \*  
37: em\_htg1: \*  
38: em\_htg2: \*  
39: em\_htg3: \*  
40: em\_htg4: \*  
41: em\_htg5: \*  
42: em\_htg6: \*  
43: em\_htg7: \*

44: em\_htg8: \*  
45: em\_htg9: \*  
46: em\_htg10: \*  
47: em\_hum3: \*  
48: em\_hum4: \*  
49: em\_hum5: \*  
50: em\_hum6: \*  
51: gb\_pi5: \*  
52: gb\_pi6: \*  
53: gb\_pi7: \*  
54: gb\_pi8: \*  
55: gb\_pi9: \*  
56: gb\_pi10: \*  
57: gb\_pi11: \*  
58: gb\_pi12: \*  
59: gb\_pi13: \*  
60: gb\_pi14: \*  
61: gb\_pi15: \*  
62: gb\_pi16: \*  
63: gb\_pi17: \*  
64: gb\_pi18: \*  
65: gb\_pi19: \*  
66: gb\_pi20: \*  
67: gb\_pi21: \*  
68: gb\_pi22: \*  
69: gb\_pi23: \*  
70: gb\_pi24: \*  
71: gb\_pi25: \*  
72: gb\_pi26: \*  
73: gb\_pi27: \*  
74: gb\_pi28: \*  
75: gb\_pi29: \*  
76: gb\_pi30: \*  
77: gb\_pi31: \*  
78: gb\_pi32: \*  
79: gb\_pi33: \*  
80: gb\_pi34: \*  
81: gb\_pi35: \*  
82: gb\_pi36: \*  
83: em\_htg0: \*  
84: gb\_pi37: \*  
85: gb\_pi38: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	100.0	591	81	A86593 Sequence 2
2	583	98.6	591	81	A86609 Sequence 18
3	581.4	98.4	591	81	A86607 Sequence 16
4	579.8	98.1	591	81	A86603 Sequence 12
5	578.2	97.8	591	81	A86601 Sequence 10
6	573.4	97.0	591	81	A86605 Sequence 14
7	558.2	94.5	605	81	AR029199 Sequence
8	447.2	75.7	2376	53	HSCRI1S
9	447.2	75.7	2376	53	G28591
10	447.2	75.7	6951	57	HSCRI1
11	445.6	75.4	1985	51	CHPCRI1X
12	445.6	75.4	6044	51	CHPCRI1WT
13	416.8	70.5	1688	51	BABCORE
14	406.4	68.8	945	51	BABCOREA
15	404.6	68.5	1731	51	CHPCRI1Y
16	399.2	67.5	6000	53	BABCR1A
17	327.2	55.4	5420	53	HSCRI1R
18	261.6	44.3	1680	11	D42115
19	261.6	44.3	1724	11	R45112
20	261.6	44.3	1811	11	R45112
21	254.4	43.0	1781	11	MUSCR1L





```
Db 301 TCACGGGCTACATGCATCATCTCTGGTGAATCTGATCTTGGGATAATGAACCCGATT 360
Qy 361 TGTGACCGAATTCCTGCTGGTCTGCGCGGACCATGCGCAACGGTGAATTCACCTCTATC 420
Db 361 TGTGACCGAATTCCTGCTGGTCTGCGCGGACCATGCGCAACGGTGAATTCACCTCTATC 420
Qy 421 AGTCGGAGTATTTTACATAGTCTGTGTGTGATCACTTACCACTGCAATCTGGGTACCGGT 480
Db 421 AGTCGGAGTATTTTACATAGTCTGTGTGTGATCACTTACCACTGCAATCTGGGTACCGGT 480
Qy 481 GGTAAAAAGGTGTTTGAAGTCTGCGGTGAGCGCTCCATCATCTAGTACAGCAAGAGCAT 540
Db 481 GGTAAAAAGGTGTTTGAAGTCTGCGGTGAGCGCTCCATCATCTAGTACAGCAAGAGCAT 540
Qy 541 CAAGTGGGCATCTGAGCGCGCCGCGACCGCAGTGCATCATCCGAAACA 591
Db 541 CAAGTGGGCATCTGAGCGCGCCGCGACCGCAGTGCATCATCCGAAACA 591

RESULT 3
A86607 591 bp DNA PAT 21-JAN-2000
LOCUS A86607
DEFINITION Sequence 16 from Patent WO9839433.
ACCESSION A86607
VERSION A86607.1 GI:6735178
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CRI)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 128 a 160 c 151 g 152 t
ORIGIN

Query Match 98.4%; Score 581.4; DB 81; Length 591;
Best Local Similarity 99.0%; Pred. No. 7.4e-172;
Matches 585; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 421 AGTCGGAGTATTTTACATAGTCTGTGTGTGATCACTTACCACTGCAATCTGGGTACCGGT 480
Db 421 AGTCGGAGTATTTTACATAGTCTGTGTGTGATCACTTACCACTGCAATCTGGGTACCGGT 480
Qy 481 GGTAAAAAGGTGTTTGAAGTCTGCGGTGAGCGCTCCATCATCTAGTACAGCAAGAGCAT 540
Db 481 GGTAAAAAGGTGTTTGAAGTCTGCGGTGAGCGCTCCATCATCTAGTACAGCAAGAGCAT 540
Qy 541 CAAGTGGGCATCTGAGCGCGCCGCGACCGCAGTGCATCATCCGAAACA 591
Db 541 CAAGTGGGCATCTGAGCGCGCCGCGACCGCAGTGCATCATCCGAAACA 591

RESULT 4
A86603 591 bp DNA PAT 21-JAN-2000
LOCUS A86603
DEFINITION Sequence 12 from Patent WO9839433.
ACCESSION A86603
VERSION A86603.1 GI:6735176
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CRI)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 134 a 158 c 146 g 153 t
ORIGIN

Query Match 98.1%; Score 579.8; DB 81; Length 591;
Best Local Similarity 98.8%; Pred. No. 2.4e-171;
Matches 584; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```

OY 481 GGTAAAGAGTGTGAGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
Db 481 GGTAAAGAGTGTGAGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
OY 541 CAAGTGGCATCTGAGAGCGCCCGGACCGCATGATCATCCGGAACAA 591
Db 541 CAAGTGGCATCTGAGAGCGCCCGGACCGCATGATCATCCGGAACAA 591

RESULT 5
LOCUS A86601 591 bp DNA PAT 21-JAN-2000
DEFINITION Sequence 10 from Patent WO9839433.
ACCESSION A86601
VERSION A86601.1 GI:6735175
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 127 a 159 c 151 g 154 t
ORIGIN

Query Match 97.8%; Score 578.2; DB 81; Length 591;
Best Local Similarity 98.6%; Pred. No. 7,6e-172;
Matches 363; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGCAGTGCACAGCTCCGGAATGAGCTCCGTCGCGCGCCGACCAACCTGATGATGAA 60
Db 1 ATGCAGTGCACAGCTCCGGAATGAGCTCCGTCGCGCGCCGACCAACCTGATGATGAA 60
OY 61 TTGAGTTCGCCGATCGTACCTACCTAGCAATAGCGCCGCGGTTATAGCGCGC 120
Db 61 TTGAGTTCGCCGATCGTACCTACCTAGCAATAGCGCCGCGGTTATAGCGCGC 120
OY 121 CGGTTTCTATCATCTGCTGTAATAAAGCTGCTGAGAGTGGTAAAGACCGTTGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAATAAAGCTGCTGAGAGTGGTAAAGACCGTTGCGA 180
OY 121 CGGTTTCTATCATCTGCTGTAATAAAGCTGCTGAGAGTGGTAAAGACCGTTGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAATAAAGCTGCTGAGAGTGGTAAAGACCGTTGCGA 180
OY 181 CGTAATCTGTGCTAATCCGCAAGATCCGTTACGCGCATGGTCAATGATCAAAAGC 240
Db 181 CGTAATCTGTGCTAATCCGCAAGATCCGTTACGCGCATGGTCAATGATCAAAAGC 240
OY 241 ATCCAGTTCGGTCCCAATTAATATCTGTGTAAGAGTTACCGTCTGATGGTTC 300
Db 241 ATCCAGTTCGGTCCCAATTAATATCTGTGTAAGAGTTACCGTCTGATGGTTC 300
OY 301 TCCAGCGCTACATCATCTCTGTGATAGTCTGATTTGGGATTAATGAACACCGATT 360
Db 301 TCCAGCGCTACATCATCTCTGTGATAGTCTGATTTGGGATTAATGAACACCGATT 360
OY 361 TGTGACGAATTCGGTGTGCTGCGCGGACCATGGCAAGGATTTACCTCTATC 420
Db 361 TGTGACGAATTCGGTGTGCTGCGCGGACCATGGCAAGGATTTACCTCTATC 420
OY 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGCAATCTGGAGCCGT 480
Db 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGCAATCTGGAGCCGT 480
OY 481 GGTAAAGAGTGTGAGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
Db 481 GGTAAAGAGTGTGAGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
OY 541 CAAGTGGCATCTGAGAGCGCCCGGACCGCATGATCATCCGGAACAA 591

```

```

Db 541 CAAGTGGCATCTGAGAGCGCCCGGACCGCATGATCATCCGGAACAA 591

RESULT 6
LOCUS A86605 591 bp DNA PAT 21-JAN-2000
DEFINITION Sequence 14 from Patent WO9839433.
ACCESSION A86605
VERSION A86605.1 GI:6735177
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Smith, R.A. and Cox, V.F.
TITLE COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL Patent: WO 9839433-A 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
FEATURES
source 1..591
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 131 a 160 c 149 g 151 t
ORIGIN

Query Match 97.0%; Score 573.4; DB 81; Length 591;
Best Local Similarity 98.1%; Pred. No. 2,5e-169;
Matches 580; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ATGCAGTGCACAGCTCCGGAATGAGCTCCGTCGCGCGCCGACCAACCTGATGATGAA 60
Db 1 ATGCAGTGCACAGCTCCGGAATGAGCTCCGTCGCGCGCCGACCAACCTGATGATGAA 60
OY 61 TTGAGTTCGCCGATCGTACCTACCTAGCAATAGCGCCGCGGTTATAGCGCGC 120
Db 61 TTGAGTTCGCCGATCGTACCTACCTAGCAATAGCGCCGCGGTTATAGCGCGC 120
OY 121 CGGTTTCTATCATCTGCTGTAATAAAGCTGCTGAGAGTGGTAAAGACCGTTGCGA 180
Db 121 CGGTTTCTATCATCTGCTGTAATAAAGCTGCTGAGAGTGGTAAAGACCGTTGCGA 180
OY 181 CGTAATCTGTGCTAATCCGCAAGATCCGTTACGCGCATGGTCAATGATCAAAAGC 240
Db 181 CGTAATCTGTGCTAATCCGCAAGATCCGTTACGCGCATGGTCAATGATCAAAAGC 240
OY 241 ATCCAGTTCGGTCCCAATTAATATCTGTGTAAGAGTTACCGTCTGATGGTTC 300
Db 241 ATCCAGTTCGGTCCCAATTAATATCTGTGTAAGAGTTACCGTCTGATGGTTC 300
OY 301 TCCAGCGCTACATCATCTCTGTGATAGTCTGATTTGGGATTAATGAACACCGATT 360
Db 301 TCCAGCGCTACATCATCTCTGTGATAGTCTGATTTGGGATTAATGAACACCGATT 360
OY 361 TGTGACGAATTCGGTGTGCTGCGCGGACCATGGCAAGGATTTACCTCTATC 420
Db 361 TGTGACGAATTCGGTGTGCTGCGCGGACCATGGCAAGGATTTACCTCTATC 420
OY 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGCAATCTGGAGCCGT 480
Db 421 AGTCGCGAGTATTTTCACTATGTTCTGTGGTGACCTACCATCGCAATCTGGAGCCGT 480
OY 481 GGTAAAGAGTGTGAGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
Db 481 GGTAAAGAGTGTGAGCTGAGTGGAGCCGCTCCATCTACTGACATAGCAAGAGCAT 540
OY 541 CAAGTGGCATCTGAGAGCGCCCGGACCGCATGATCATCCGGAACAA 591
Db 541 CAAGTGGCATCTGAGAGCGCCCGGACCGCATGATCATCCGGAACAA 591

```

AR029199  
 LOCUS AR029199 605 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 33 from patent US 5859223.  
 ACCESSION AR029199  
 VERSION AR029199.1 GI:5941172  
 KEYWORDS  
 SOURCE  
 ORGANISM Unknown.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 605)  
 Mossakowska,D.Ewairena, Dodd,I., Freeman,A.Mary and Smith,R.AnthonyGodwin.  
 TITLE Soluble CRI derivatives  
 JOURNAL Patent: US 5859223-A 33 12-JAN-1999;  
 FEATURES  
 source Location/Qualifiers  
 1..605  
 /organism="unknown"  
 BASE COUNT 136 a 161 c 150 g 158 t  
 ORIGIN

Query Match 94.5%; Score 558.2; DB 81; Length 605;  
 Best Local Similarity 97.6%; Pred. No. 1.5e-164;  
 Matches 577; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 1 ATGCGATGCAAGCGTCCGGAATGCGTCCGCGCCGCCGCAACCTGACTGATGA 60  
 DB 4 ATGCGATGCAAGCGTCCGGAATGCGTCCGCGCCGCCGCAACCTGACTGATGA 63  
 QY 61 TTGAGTTCGCCATGCGGTACTGACTGACTGACTGACTGACTGACTGACTGACT 120  
 DB 64 TTGAGTTCGCCATGCGGTACTGACTGACTGACTGACTGACTGACTGACTGACT 123  
 QY 121 CCGTTTTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 DB 124 CCGTTTTCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183  
 QY 181 GCTAATCTGTCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 DB 184 GCTAATCTGTCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243  
 QY 241 ATCCAGTTCGTTCCCAATTAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 DB 244 ATCCAGTTCGTTCCCAATTAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303  
 QY 301 TCCAGCGTACATGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 DB 304 TCCAGCGTACATGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363  
 QY 361 TGTGACCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 DB 364 TGTGACCGAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423  
 QY 421 ACTCGGATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 DB 424 ACTCGGATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483  
 QY 481 GGTAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 DB 484 GGTAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543  
 QY 541 CAAGTGGGATCTGAGAGCGCGCGGACCGACGAGTGCATCATCCGGAACAA 591  
 DB 544 CAAGTGGGATCTGAGAGCGCGCGGACCGACGAGTGCATCATCCGGAACAA 593

RESULT 8  
 HSCRIAS  
 LOCUS HSCRIAS 2376 bp mRNA PRI 22-MAR-1995  
 DEFINITION Human CRI mRNA for C3b/C4b receptor secreted form.  
 ACCESSION X14362.Y00812  
 VERSION X14362.1 GI:30197  
 KEYWORDS alternate splicing; C3b/C4b receptor; complement receptor;

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 2376)  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-1988) Hourcade D., Howard Hughes Medical Institute, 660 S. Euclid St. Louis Mo, 63110, USA  
 REFERENCE  
 AUTHORS 2 (bases 1 to 2376)  
 TITLE Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1  
 JOURNAL J. Exp. Med. 168 (4), 1255-1270 (1988)  
 MEDLINE 89010527  
 COMMENT The sequence overlaps with that reported by Klickstein et. al. in J. Exp. Med. 165:1095-1112(1987) x05309 and in J. Exp. Med. 168:1699-1717(1988).  
 FEATURES  
 source Location/Qualifiers  
 1..2376  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /haplotype="CRI-A"  
 /cell\_line="HL-60"  
 /clone="CRI-4"  
 <1..1682  
 /note="CRI receptor precursor (AA -16 to 543) (1 is 2nd base in codon)"  
 /codon\_start=3  
 /protein\_id="CAA32541.1"  
 /db\_xref="GI:736240"  
 /translation="SLAVVVVLLALPVAGOCNAPEMLPFAPPTLIDFEFPIGYL  
 NTEPRGSGRPSIIICLKNSTVGAKRCRCRSCRNPPDPVNGAVHIKGIQFSGOI  
 KYSCIKRGLIGSSATCIISGDVIMYINENPIDCRIGCGIPPTTNDDFTSTNENF  
 HVSQVYTRCRNPGSGRKYFELNPSIYCNENSDOVINSRPAQCIIIPKPKTPNV  
 ENGLIVSNRSLFSLNEVERFCQGFVMAKGRKVCOLKNKEPELSCSVQCPP  
 DVLAHERQORDNFSPGQEVFVSCPEYDLDGAASMCCTPQGDMSPAAPCEVSCD  
 DFMQGLNGLRVLFVNLQIAKVFVCDGEFQKSSASVCLVLAGMESLWMSVAVCE  
 QIFCPSPVPINGRHTGKPLFVFPGRKAVNTCDPHDPDRGTSLDLSGTIRCTSDPQ  
 GNGVWSPAPRGIGIHCQAPDHFALFKTQTNASDPDPIGSLKYECRPRYGRPS  
 ITCDLNLYWSSPKVCKRKSCKTPDPVNGAVHVTIDQVSRINVSCTTG"  
 <1..50  
 /product="signal peptide (AA -17 to -1) (1 is 2nd base in codon)"  
 mat\_peptide 51..1679  
 /product="mature CRI receptor (AA 1-543); secreted form"  
 polyA\_site 2376  
 /note="polyA site"  
 BASE COUNT 633 a 549 c 568 g 626 t  
 ORIGIN

Query Match 75.7%; Score 447.2; DB 53; Length 2376;  
 Best Local Similarity 85.0%; Pred. No. 1.4e-129;  
 Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 4 CAGTGCACGCTCCGGAATGCGTCCGCGCCGCCGCAACCTGACTGATGAATT 63  
 DB 51 CAGTGCACGCTCCGGAATGCGTCCGCGCCGCCGCAACCTGACTGATGAATT 110  
 QY 64 GAGTTCGCCATGCGGTACTGACTGACTGACTGACTGACTGACTGACTGACTGACT 123  
 DB 111 GAGTTCGCCATGCGGTACTGACTGACTGACTGACTGACTGACTGACTGACTGACT 170  
 QY 124 TTTTCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183  
 DB 171 TTTTCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230  
 QY 184 AATATCTTGCTGAATCCGCGAGATCCGCTTAACGCGATGCTGATGATCAAGGATC 243  
 DB 231 AATATCTTGCTGAATCCGCGAGATCCGCTTAACGCGATGCTGATGATCAAGGATC 290

Buffer:	
MgCl <sub>2</sub> :	2.5 mM
KCl:	50 mM
Tris-HCl:	20 mM
pH:	8.3

REFERENCE 1 (bases 1 to 6951)

AUTHORS      Klickstein L.B.  
TITLE        Direct Submission  
JOURNAL     Submitted (20-OCT-1998) Klickstein L.B., Room 617 Hunterian Bldg.,  
             725 N. Wolfe St., Baltimore, MD 21205  
REFERENCE   2 (bases 1 to 1531)  
AUTHORS     Klickstein L.B., Bartow, T.J., Millett, Y., Radson, L.D., Smith, J.A.  
             and Fearon, D.T.  
TITLE        Identification of distinct C3b and C4b recognition sites in the  
             human C3b/C4b receptor (CRI, CD35) by deletion mutagenesis  
JOURNAL     J. Exp. Med. 168 (5), 1699-1717 (1988)  
MEDLINE     89035992  
COMMENT     This is the sequence of the F allele type of CRI.  
             seq pos. 1532-6951 are already reviewed see x05309 Data kindly  
             reviewed (16/5/89) by Klickstein L.  
FEATURES  
source       1. 6951  
             /organism="Homo sapiens"  
             /db\_xref="taxon:9606"  
             /tissue\_type="tonsil and HL-60"  
             /clone\_1lb="lambda S2T (ATCC #37546)."  
sig\_peptide   28..150  
             /product="signal peptide (-41 to -1)"  
             28..6147  
             /note="CRI precursor protein"  
             /codon\_start=-1  
             /protein\_id="CA6875.1"  
             /db\_xref="GI:30186"  
             /db\_xref="SWISS-Prot:P17927"  
             /translation="MGASSPRSEPEVPGVAPGAPGPGCGSILAVVLLAPVAMGOCN  
             APMLPAPRTNLTDEFEPPIGYLNECEPGSGPSTICLNSTWTKACRKRK  
             SCRNPDVPGVAVHVKIGIOFSQIKYSCGKRLIGSSATNCTIIGDPTNEMPI  
             CDRIIPGRLTNGDSTINRNPHKSVYTRCNRGSGRGTIELVGGPSTYCSN  
             DDVGTFMSGPAPCCITPNKCTPPNVEGILVSDNRSLFSLNEVEVERSCQGEYFVAKGPR  
             RYKQALNKEPELPSCSRVCPDPVLAERQKDNPPSCQGEYFVSCQEDYDAG  
             AAMRCITPOGDMGAPATCEVSKCDDEMGQLNGRVLPVNLQAKVDPVCEGEFOL  
             KSSASVYLAEMSESLNMSVPCVEQIFCSPPIVPGRIHGTGLAEVFPKQAVNTC  
             DPHBDSITDILGESIRICTSDPGGWSPPARVCGILGHQADPHFTLAKTQF  
             MASDPICSTLAKCEPREYGRPFSTICLDNLVSSKDYCKRCKSTPPDPYNGVH  
             VIIDIVGSRINTSCITGHRILGHSSNECLISGNAAWSTKPIQRIPOGSLPTIAN  
             GDFISTNRENFHGSVYTRCNPNGSGRKFELVGEPSICTSDNDVGTMSGPAPQC  
             ILPNKCTPPNVEGILVSDNRSLFSLNEVEVERSCQGEYFVAKGPRYKQALNKEPEL  
             PSCSRVCPDPVLAERQKDNPPSCQGEYFVSCQEDYDAGVLAASMRCTPOGDMSP  
             AAPTCEVSKCDDEMGQLNGRVLPVNLQAKVDPVCEGEFOLKSSASVYLAEME  
             SLNMSVPCVEQIFCSPPIVPGRIHGTGLAEVFPKQAVNTCDDPHBDSITDILGE  
             ESTIRCTSDPGGWSPPARVCGILGHQADPHFTLAKTQJNMSDFIGSLYKE  
             CREYIGRPFSTICLDNLVSSPKDYCKRCKSTPPDPVNGVHVIIDIVGSRINTS  
             CTGHRILGHSSNECLISGNAAWSTKPIQRIPOGSLPTIANGDFISTNRENFHGS  
             SVYTRCNPNGSGRKFELVGEPSICTSDNDVGTMSGPAPCCITPNKCTPPNVEG  
             IIVSDNRSLFSLNEVEVERSCQGEYFVAKGPRYKQALNKEPELPSCSRVCPDPV  
             HGHRTPSHQDNFSPQGEYFVSCQEDYDAGVLAASMRCTPOGDMSPDEAPRCVAKSCDDE  
             GQPHGRVLPVNLQAKVSEVCEGFRUKGSSVSHCVLVGKRSIMNNSVPCGEHFG  
             CPMPPAILNGRHTGTPSGDIPYKEISITYPDIPNDEFPVGTLANECRGYFKMES  
             WMSPPARCELSVIRACHAKTPEQPFASPTIPINDEFPVGTLANECRGYFKMES  
             ISCELENVMSVEDNCRKSGCPPEPFENMHVINDTQGSTVNSCNGEFLISP  
             STICLVSGNNVTDKKAPICEIISCEPPIISGDFENNRNTEPHNCTVYTCOCHGP  
             DGOQLFEIYGERSTICTSKDVOGWSPPRCPSTINRKTAPVEMIRVAPGRSFTS  
             LHEILIRCPQGEVWVGSHTVQCOTGRMSPKIPHCGRVCPQPELHGHSTLSDND  
             FSPGOEVYFSCPEPSYDLRGASLHCTPOGWSSEAPACVYKSCDDEFGQPHGRVLP  
             LNLQAKVSEVCEGFRUKGSRASHVLGMAALNMSVPCVEQIFCQPMPPAILNR  
             HTGTPEGDIPIYKEISVACDHPDRGMTFNLIJESSIRCSJSDNOGWSPPARCELS  
             SVAPACHPKRIQNGHYIGGHSVILPQMTIYSTCDGTVLVCAGTFCFCDQIMSLD  
             DHYCKEYVCSFPLPMNGISKELEMKRYHHGADVTLKCEGTYLLEBSPQCCADDNM  
             DPLAKCTSRADHALYVGTISGTIFLLITLIFSWILLKRRKNAMENKEVAIHLH  
             SGGGSSVHPRTIDTNEHSRVLPP  
mat\_peptide   151..6144  
             /product="mature CRI protein (AA 1-1998)."  
             151..1500  
             /note="long homologous repeat A coding sequence"  
             1501..2850  
             /note="long homologous repeat B coding sequence"  
             2851..4209  
             /note="long homologous repeat C coding sequence"  
             4210..5565  
misc\_feature   misc\_feature  
             misc\_feature

BASE COUNT      1802 a      1680 c      1661 g      1808 t  
ORIGIN  
Query Match      75.7%; Score 447.2; DB 53; Length 6951;  
Best Local Similarity 85.0%; Pred. No. 1.4e-129;  
Matches 500; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
             /note="long homologous repeat D coding sequence"  
             ORIGIN  
QY      4    CAGTCAACCGCTCCGAGATGGCTGCGCGCGCCGCAACCACTGATGATGATTT 63  
             || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||  
DB      151    CAATGCAATGCCAGATGGCTTCCATTGGCCAGGCTTCAACCACTGATGATTT 210  
QY      64    GAGTCCCGATCGGTACTTACCTGACTGACGATGCCCGCGGTATPAGCGCCCGC 123  
             ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||  
DB      211    GAGTTCCCATGGGACATCTGAACTAGAAATGACCGCCCTGGTTATTCGGGAAGCCG 270  
QY      124    TTTTCTATCATCTGCCGAAAACTCTGCTGACGTGGTCTAAGACCGTTGCCGACGT 183  
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      271    TTTTCTATCATCTGCCGAAAACTCTGCTGACGTGGTCTAAGACAGGTGACGACGT 330  
QY      184    AAATCTGTGCTATCCGCGAGATCCGTTACGCGCATGGTGCATGATCAAGGCATC 243  
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      331    AAATCATGTGTATATCTCCAGATCCTGTAAGSGCATGGTGCATGATCAAGGCATC 390  
QY      244    CAGTTCGTTCCCAATTAATATCTTGTACTTAAAGGTTACCGTCTGATGGTCTCC 303  
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      391    CAGTTCGATCCCAATTAATATCTTGTACTTAAAGGTTACCGATCATGGTCTCTCG 450  
QY      304    AGGCTCATGATCATCTCTGGTATACGTCTTTGGGATATGAACACGATTTGT 363  
             || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      451    TCTGCATCATGATCATCTCTAGGTATAGTCTTTTGGGATATGAACACCTATTGT 510  
QY      364    GACCAATTCCTGTGTGCTGCGCGCCGACCATCGCAACGGTATTTACCTTATCAT 423  
             || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      511    GACGAATTCCTGTGTGCGTACCCCGACCATGACCAATGAGATTTACATGACACA 570  
QY      424    CGCGATATTTTACATATGTTGTGTGTGACCTTACCATGTCAATCTGGGTAGCGGT 483  
             || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      571    AGAAGATTTTCTACTATGATCAGTGTGACCTTACCATGTGGAAGGAGGAGG 630  
QY      484    AAAAGGTGTTTGGTGCCTGGGTGACCGCTTCACTACGCACTACCAAGAGATGAA 543  
             || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      631    AGAAGGTGTTTGGTGCCTGGGTGACCGCTTCACTACGCACTACCAAGATGAA 690  
QY      544    GTGGGCACTTGAGCGCGCGGACCGCATGCTATCCGGAACAA 591  
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
DB      691    GTGGGCACTTGAGCGCGCGCGCATGCTATTACTTAACAA 738  
RESULT 11  
CHPCR1X  
LOCUS      CHPCR1X      1985 bp      mRNA      PRI      30-OCT-1994  
DEFINITION      Pan troglodytes alternatively spliced CRI (CRI) gene, partial cds.  
ACCESSION      U24921.1      GI:557726  
VERSION      124921.1      GI:557726  
KEYWORDS      alternative splicing product; complement receptor 1.  
SOURCE      Pan troglodytes  
ORGANISM      Pan troglodytes  
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE      1 (bases 1 to 1985)  
AUTHORS      Mammalian, D.J., Shen, X.P., Hourcade, D., Nickells, M.W. and  
             Ackinson, J.P.  
TITLE        Primary sequence of an alternatively spliced form of CRI. Candidate  
             for the 75,000 M(r) complement receptor expressed on chimpanzee  
             erythrocytes  
JOURNAL     J. Immunol. 153 (2), 691-700 (1994)  
MEDLINE     94292799  
FEATURES  
source       1. 1985  
             /organism="Pan troglodytes"  
             /db\_xref="taxon:9598"  
             Location/Qualifiers



Query Match	75.4%	Score 445.6	DB 51	Length 6044
Best Local Similarity	84.9%	Pred. No. 4,5e-121		
Matches 499	Conservative	0	Mismatches 89	Indels 0
Gaps				0

OY	4	CAGTCAACGCTCCCGAATGGCGCTGTGGCGGCCCGCACCACTGCATGATATT	63
Db	51	CATTCGATGGCCCCAGAATGGCTTCCATTGTGCCAGGCCCTACCACTCATATGATT	110
OY	64	GAGTTCCGATGGGTACTCCTGAACCTAAGATGGCCGCCGGGTTATAGCGGCCG	123
Db	111	GAGTTCCCATTTGGGACAATATCTGAACATATGATGGCCGCCCTGTGTTATATGAAAGACCG	170
OY	124	TTTTTATCATCTGGCTGAAAACCTCTCTGTGATCTGTGTCTTAAGACCGCTGCCAGCT	183
Db	171	TTTTTATCATCTGGCTATAAAAACTCAAGCTGAGTGGTGCTAAGACAGGTGCAAGCT	230
OY	184	AAATCTTGCGTAATCCCGCAGATCCGGTTAACGGCATGTGCATGTGATCAAAGCATC	243
Db	231	AAATCATGTGCGTAATCTCCACATCTCTGGAATGGCATGTGTGATCTCAAGCATC	290
OY	244	CAGTTGGTTCCCAATTAATATTTCTGTACTAAAGGTTACCCTGTGATTTGTTCTCC	303
Db	291	CAATTCGGATCCCAATTAATATTTCTGTACTAAAGATACGCATCATGTGTTCTCTG	350
OY	304	AGCGTACATGATATATCTCTGTGATATGTGCATTTGGGATAATGAACCCAGATTGT	363
Db	351	TCTGTCACATGGATATATCTCAGGTGTACTGTGCATTTGGGATAATGAACACCTATTGT	410
OY	364	GACCAATTCCTGTGTGTGTCGCCGCGACCATCGCCAAAGGATTTACCTCTATCACT	423
Db	411	GACCAATTTCTGTGTGTGTCGCCGCGACCATCGCCAAAGGATTTACCTCTATCACT	470
OY	424	CGCGATATTTTCACTATGTTCTGTGTGATACCTACCACTGCATCTGGGATGGTGT	483
Db	471	AGAGAGAAATTTTCACTATGATGATCAGTGTGATACCTACCGTGCATCTGGGATGGG	530
OY	484	AAAAAGGTGTGACTCGTGGGTGAAGCCGTGCATCTACTGCACTAACAAGCATCA	543
Db	531	AGAAAGGTGTGTGACTGTGTGGTGAAGCCCTGCATCTACTGCAACGCAATGACATCA	590
OY	544	GTGGCATCTGGAGGCGCCGCGACCGCATGTCATCATCCGAACAA	591
Db	591	GTGGCATCTGGAGGCGCCGCGACCTCATGTCATCATCTACCAAA	638

RESULT 13	BABCORE LOCUS	BARCODE	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE AUTHORS	JOURNAL FEATURES
	L77977.1 GI:1301608	1688 bp mRNA	Papio cynocephalus complement receptor mRNA, partial cds.	L77977	complement C3b; complement receptor; glycoposphatidylinositol-linked protein.	Papio cynocephalus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Papio	Birmingham, D.J., Logan, C.M., Shen, X.-P. and Chen, W. The baboon erythrocyte complement receptor is a glycoposphatidyl inositol-linked protein encoded by a homologue of the human CRI-like genetic element unpublished (1996)	Location/Qualifiers l. 1688 /organism="Papio cynocephalus" /db_xref="taxon:9556" /cell_type="erythrocyte" /dev_stage="adult" /tissue_type="bone marrow"  

MRNA	CDS
<1..1571	

			/note="homologue of human CRI-1-like genetic element"
			/codon_start=3
			/product="complement receptor"
			/protein_id="AA99004.1"
			/db_xref="GI:1301609"
			/translation="vvyQRKGASSPRSPREYVGPAPALLFCCGGSLAVVYLALPVA WGQCNAPQLPFARPLNLTLDASEPFTVITYKEDLPYHKKPSIIICLNKSVTASD KCCKRSKNRKPDPVNGMVAHYIKDIQFSQJNSCNMKYRLIGSSSAICIIISGTVIND NEPEICIIIFCGLPTIANGDLISTRESYPVGVVYRNLAGSRKLELVGEPSI YCISKDOVGIMSGPAPQCIIIPNKCMPEINENGVLVYNLSFLNVEFFRCOPGV MKGRHHOCCALMWELPELPCSCRVCPPEILITAGETSHOEPSPGOVFCEBCE DLRAAALHCTPGQDNMPLEAPICTVCACDFLLQGLPHGRVLPFLNLQGLAKVSFCDE GFRIKGFASHCVIAKGKALMNSSVPACEDIFCPNPAIILNGRIAGLPIDIPKGV SYIEDPPDRGMTVNLIIGESTIRCTSDPOGNWMSAPRCELSPVAGADDAIVGTL SGTFVILFIIFLFS"
BASE COUNT	413 a	427 c	411 g 437 t
ORIGIN			
Query Match	70.5%;	Score 416.8;	DB 51; Length 1688;
Best Local Similarity	81.8%;	Pred. No. 5e-120;	
Matches 481;	Conservative 0;	Mismatches 107;	Indels 0; Gaps 0;
OY	4	CAGTGCAACGCTCCGGAAATGGCTGCCGTTCGGCGCGCCCGACCAACTGCATGTAATT	63
Dd	141	CAATCAATGCCCCCGAACAGACTTCATTTCCAGCGCTACCACAACCTAGATGCATCT	200
OY	64	GAGTCCCGCATCGGACCTGACCTGAACAGAAAGCCCGCGGGTTAAGGGCGCGCCG	123
Dd	201	GAGTTTCCCCTTGGGACATATCTGAAGTAGATAGATGCTCCCTGGTTATCATGAAACCA	260
OY	124	TTTTCTATCATCTGCGCTGAAAAAACHCTGCTGTGAGATGGTGTGTAAGSACCTGTTCGACGT	183
Dd	261	TTTTCTATCATCTGCGCTAAAAAAAGTCACTGTGAGCAATGCTGAAGCAAAAGTGCACAGCT	320
OY	184	AAATTTGTGCTAATCCGCCAGATCCGTTAAAGCGCATGTGTCATGTATCAAAGCATC	243
Dd	321	AAATCATGTCTGAATCCCTAAAGATCCTGTGAATGAGCATGTGATCAAGAAGACATC	380
OY	244	CAGTTCCGTTCCCAATTAATTAATTCCTGTGCTAAGTTACCGCTGATGGTTCCGCC	303
Dd	381	CAGTTCCGATCCCAATTAATTAATTCCTGTGATAAAGGATACCGACTGATTTGTTCCTCG	440
OY	304	AGCGCTACATGATCATCTCTGTGTGATAGTGTCAATTTGGATTAAGAAACACGATTGT	363
Dd	441	TCCGCCACATGATATATCTCAGGCAATCTGTGATTTGGATTAAGAAACACATATTGT	500
OY	364	GACCGAATTCGCTGTGCTGCGCCGCGACCATCCGCAAGSGTGATTTCACCTTATCACT	423
Dd	501	GAGATTAATTCCTTGTGGGCTCACCCCCACCAATCCGCAATGAGATTCATTAGACACAGC	560
OY	424	CGCGGATTTTTCTACATAGTTCTGTGTGTGACCTAACCCTGCATCTGGGTAGCCGTGT	483
Dd	561	AGAGATGATTTTCTCCTACGAGATCCGTGTGACTTATCCCTCCAATCTTGGAAGCGGAAG	620
OY	484	AAAAAGAGTTTGAAGCTGTGGGTAGCGCTGCATCTACTGCATAGCAAGACAGATCAA	543
Dd	621	AAAAAGAGTTTGAAGCTGTGGGTAGCGCTGCATCTACTGCATAGCAAGACAGATCAA	680
OY	544	GTGGGCATCTGGAGCGCGCCGCGACCGCATGTCATATCCGGAACAAA	591
Dd	681	GTGGGCATCTGGAGCGCGCCGCGCCCTCAGTGCAATTATTAACCAACAAA	728
RESULT 14			
BABCOREA			
LOCUS	BABCOREA	945 bp	mRNA
DEFINITION	Papio cynocephalus complement receptor mRNA, partial cds.		
ACCESSION	L77978		
VERSION	L77978.1	GI:1301610	
KEYWORDS	complement C3b; complement receptor; glycoposphatidylinositol-linked protein. Papio cynocephalus cdna to mRNA.		
SOURCE			

ORGANISM Papio cynocephalus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Papio.  
REFERENCE 1 (bases 1 to 945)  
AUTHORS Birmingham D.J., Logar C.M., Shen X.-P. and Chen W.  
TITLE The baboon erythrocyte complement receptor is a glycoposphatidyl  
inositol-linked protein encoded by a homologue of the human  
CRI-1-like genetic element  
JOURNAL Unpublished (1996)  
FEATURES  
source Location/Qualifiers  
1..945  
/organism="Papio cynocephalus"  
/db\_xref="taxon:9556"  
/cell\_type="lymphocyte"  
/dev\_stage="adult"  
/tissue\_type="bone marrow"  
CDS  
mRNA  
CDS  
/note="homologue of human CRI-1-like genetic element"  
/product="complement receptor"  
/protein\_id="AAA99005.1"  
/db\_xref="GI:1301611"  
/translation="QCNAPQLPAPRPTELIDSEFSIGHLYECPGPGYRPSII  
CLNSVWTSANDRCIRKSRNPDPVNGWVHVKIDQFQSOIYVSCTEGRLIGSSA  
TCIISGNTYIMDNERTPICRISGLPTINDNGFVSKNKEFYHGVVYVYRNLGSG  
RKLFELVGPSTVYCSNEDQVWISGAPQCIIPNCTPNNENGVIVNRSLESLN  
EYVERPCRGPFYMKGRPRVCOQALNKWPELPSGRVCPDPVHLGERTQDRDIFQ  
TGOEVFYIEPSTYDRGASLRCTPDGMSAPRCEVYK  
BASE COUNT 252 a 224 c 228 g 239 t 2 others  
ORIGIN

Query Match 68.8%; Score 406.4; DB 51; Length 945;  
Best Local Similarity 80.4%; Pred. No. 9.3e-117;  
Matches 473; Conservative 2; Mismatches 113; Indels 0; Gaps 0;

4 CAGTGCACGCTCGGGAATGCTGCGTGGCGCCGCGCAACCTGACTGATGATTT 63  
1 CAAATGCAATGCCCCGGAACAGCTTCCATTTGCCAGGCCCTACGAACTAATGATGACT 60  
64 GAGTTCCGATCGTACTACTGAACTAGAAATGCGCCGCGGTATAGCGCCGCCG 123  
61 GAGTTTCCATGGGACACATCTGAAGTATGATGACGCGCTGTTATATGGAAGACR 120  
124 TTTTCTATCATCTGCTGAAAACTCTGCTGACTGCTGCTAAGACCGTTGCCGAGT 183  
121 TTTTCTATCATCTGCTGAAAACTCTGCTGACTGCTGCTAAGACCGTTGCCGAGT 180  
184 AAATCTGTGCTATCGCGAGATCGGGTAAAGGATGCTGATCAAGGATC 243  
181 AAATCATGTCTATCTCTAGAGATCTGTGATGATGATGATGATCAAGGATC 240  
244 CAGTTGCGTCCCAATTAATATCTGTTGACTAAGATTAACGCTGATGTTGCTCC 303  
241 CAGTTGCGTCCCAATTAATATATCTGTTGACTAAGATTAACGCTGATGTTGCTCA 300  
304 AGCGCTACATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 363  
301 TCTGACATCATCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 360  
364 GACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423  
361 GAGAAATTTCTTGTGGGCTACCAACCCATAGACAAAGGATTTCTTATGCTAAC 420  
424 CGCGAGATTTTCACTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 483  
421 AAAGAGATTTTCACTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480  
484 AAAAGGATTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAG 543  
481 AGAAAGCTTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAG 540

544 GTGGCATCTGGAGCGCCGCGCAGCAGCATGATCATCCGACAAA 591  
541 GTGGCATCTGGAGCGCCGCGCAGCAGCATGATCATCCGACAAA 588

RESULT 15  
LOCUS CHPCR1Y 1731 bp mRNA PRI 12-OCT-1994  
DEFINITION Pan troglodytes mRNA sequence, 3' end of ORF.  
ACCESSION L24922  
VERSION L24922.1 GI:557728  
KEYWORDS  
SOURCE  
ORGANISM Pan troglodytes cDNA to mRNA.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
REFERENCE 1 (bases 1 to 1731)  
AUTHORS Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W. and  
Atkinson V.P.  
TITLE Primary sequence of an alternatively spliced form of CRI. Candidate  
for the 75,000 M(r) complement receptor expressed on chimpanzee  
erythrocytes  
JOURNAL J. Immunol. 153 (2), 691-700 (1994)  
FEATURES  
MEDLINE  
source Location/Qualifiers  
1..1731  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/cell\_line="EBV transformed"  
/cell\_type="B cell"  
CDS  
1571..>1731  
/note="Possible homologue to human CRI-1-like genomic  
element"  
/codon\_start=3  
/protein\_id="AA50460.1"  
/db\_xref="GI:557729"  
/translation="DEFEPIGTYLNEYCPGPGYRPSIICLNKSVTSADCKRX  
SCRNPDPVNGWVHVKIDQFQSOIYVSCTEGRLIGSSATCIISGNTYIMDNKIPV  
CDRIICGLPTINDNGFVSKNKEFYHGVVYVYRNLGSGRKLFELVGPSTVYCSNEDQVWISGAPQCIIPNCTPNNENGVIVNRSLESLN  
EYVERPCRGPFYMKGRPRVCOQALNKWPELPSGRVCPDPVHLGERTQDRDIFQ  
TGOEVFYIEPSTYDRGASLRCTPDGMSAPRCEVYK  
SYTCDPDRDGMTFNLIESTIRCTSDPDRGMSWSPAPRCELVGASDPAIVGTL  
LGIIIFIIIIIFLY"  
BASE COUNT 469 a 395 c 403 g 463 t 1 others  
ORIGIN

Query Match 68.5%; Score 404.6; DB 51; Length 1731;  
Best Local Similarity 84.4%; Pred. No. 3.5e-116;  
Matches 453; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

53 CTGATGAATTTAGATTCGCGATCGGTACTGATGAACTAGAAATCCGCCCGGTTATA 112  
1 CTGATGAATTTAGATTCGCGATCGGTACTGATGAACTAGAAATCCGCCCGGTTATA 112  
113 CGGCGCGCGCGTCTTATCATCTGCTGAAAACTCTGCTGAGATGGGCTAAGAGAC 172  
61 ATGGAAGACATTTTCTATCATCTGCTGAAAACTCTGCTGAGATGGGCTAAGAGAC 120  
173 GTTCCGAGCTAATCTGCTAATCCGCAATCCGCTTAAGCGATGCTGATGCA 232  
121 AGTGCAAACCTAATATCTGCTAATCCGCAATCCGCTTAAGCGATGCTGATGCA 180  
233 TCAAGGATCATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292  
181 TCAAGGATCATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
293 TTGCTCTCCAGCGCTAATGATCATCTCTGCTGATGCTGCTGCTGCTGCTGCTGCT 352





**THIS PAGE BLANK (USPTO)**



PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
PT used to treat disorders and diseases associated with inflammation or  
XX inappropriate complement activation  
PS Claim 13; Page 42; 67pp; English.  
XX  
CC This is the amino acid sequence of CM7, a protein that consists  
CC of the short consensus repeats (SCR) 1 and 2 from the complement  
CC receptor type 1 (CRI) fused to the SCR3 of CRI-like protein (see  
CC W9247). CM7 DNA (see V53262) was constructed using pDB1013-5,  
CC which codes for SCR1-3 of CRI, by site-directed mutagenesis that  
CC resulted in the introduction of 10 amino acid changes to the native  
CC SCR3 sequence corresponding to changes observed in the protein  
CC encoded by the CRI-like pseudogene (Cripse). The DNA construct  
CC in plasmid pProcCR1-3CM7 was used to transform *Escherichia coli*  
CC BL21(DE3) cells, and CM7 was purified from solubilised inclusion  
CC bodies. The invention provides DNA sequences (see V53262 and  
CC V53269-79) encoding novel soluble engineered CRI polypeptides (see  
CC W53236-47) such as CM7 that act as complement inhibitors with  
CC functional complement inhibitory, including anti-haemolytic,  
CC activity. These can be used to treat a disease or disorder  
CC associated with inflammation or inappropriate complement activation,  
CC such as neurological disorders (e.g. multiple sclerosis and  
CC Parkinson's disease), disorders of inappropriate or undesirable  
CC complement activation (e.g. xenograft rejection), inflammatory  
CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
CC post-ischaemic reperfusion conditions, infection or sepsis,  
CC immune complex disorders and autoimmune diseases (e.g. rheumatoid  
CC arthritis, proliferative nephritis and myasthenia gravis), and  
CC reproductive disorders.  
XX  
SQ Sequence 197 AA;  
  
Query Match 100.0%; Score 1104; DB 19; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2, 4e-99;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MQCNAPFWLPAPRTNLTFDEFFPIGTLYLNECRPGYSGRPFSTICLNQSVWTGAKDKCR 60  
DB 1 mqcnapewlpfarpnltdfeffpigtlylneecrpgysgrpfsticlnqsvwtgkdkrcr 60  
  
QY 61 RKSCRNPDPVNGVHWIKIGIOFGSQIKYSCCTKGYRLIGSSATCITISGTVIWNDETPI 120  
DB 61 rkscrnpdpvngvhwikigiofsgsqikyscctkgyrllgssatcitsgdtviwneetpi 120  
  
QY 121 CDRIPCGLPPTIANGDFTSISREYFHGVSVTYHCNLSGRGKVFELVGEPSITCTSKDD 180  
DB 121 cdripcglpptiangdftsisisreyfhgvsvtyhcnlsgrgkvfelvgepsitctskdd 180  
  
QY 181 QVGIMSGPAPQCIIPNK 197  
DB 181 qvgiwsgapqciipnk 197  
  
RESULT 2  
W75986 W75986 standard; Protein; 198 AA.  
XX  
AC W75986;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Complement receptor type 1-like polypeptide CM7/Cys.  
XX  
KM Complement receptor type-1; CRI; CM7/Cys; complement; inhibitor;  
KM anti-haemolytic; multiple sclerosis; Parkinson's disease;  
KM xenograft rejection; inflammation; Crohn's disease; asthma;  
KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
KM myasthenia gravis; reproductive disorder; therapy.  
XX  
OS Homo sapiens.

OS Synthetic.  
XX  
PN WO9839433-A1.  
XX  
XX 11-SEP-1998.  
PD  
XX  
XX 05-MAR-1998; 98WO-GB00727.  
PF  
XX  
XX 05-MAR-1997; 97GB-0004519.  
PR  
XX  
PA (ADPR-) ADPROTECH PLC.  
XX  
XX Cox VE, Mossakowska DEI, Smith RAG;  
PI WPI; 1998-506358/43.  
DR  
XX  
XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
PT used to treat disorders and diseases associated with inflammation or  
PT inappropriate complement activation  
PS Claim 19; Page 51-52; 67pp; English.  
XX  
XX This is the amino acid sequence of CM7/Cys, a protein that consists  
XX of the short consensus repeats (SCR) 1 and 2 from the complement  
XX receptor type 1 (CRI) fused to the SCR3 of CRI-like protein (see  
XX W9247) and having an additional C-terminal Cys residue. CM7/Cys  
XX DNA was constructed by site-directed mutagenesis (see V53280)  
XX of pProcCR1-3CM7 (see V53262). This plasmid was used to transform  
XX *Escherichia coli*, and CM7/Cys was purified from solubilised  
XX inclusion bodies. The invention provides novel soluble engineered  
XX polypeptides (see W53236-47 and W75986-94) such as CM7/Cys that act  
XX as complement inhibitors with functional complement inhibitory,  
XX including anti-haemolytic, activity. These can be used to treat a  
XX disease or disorder associated with inflammation or inappropriate  
XX complement activation, such as neurological disorders (e.g.  
XX multiple sclerosis, Parkinson's disease), disorders of inappropriate  
XX complement activation (e.g. Crohn's disease, asthma, and acute  
XX inflammatory disorders (e.g. Crohn's disease, asthma, and acute  
XX pancreatitis), post-ischaemic reperfusion conditions, infection or  
XX sepsis, immune complex disorders and autoimmune diseases (e.g.  
XX rheumatoid arthritis, proliferative nephritis and myasthenia  
XX gravis), and reproductive disorders.  
XX  
SQ Sequence 198 AA;  
  
Query Match 100.0%; Score 1104; DB 19; Length 198;  
Best Local Similarity 100.0%; Pred. No. 2, 4e-99;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MQCNAPFWLPAPRTNLTFDEFFPIGTLYLNECRPGYSGRPFSTICLNQSVWTGAKDKCR 60  
DB 1 mqcnapewlpfarpnltdfeffpigtlylneecrpgysgrpfsticlnqsvwtgkdkrcr 60  
  
QY 61 RKSCRNPDPVNGVHWIKIGIOFGSQIKYSCCTKGYRLIGSSATCITISGTVIWNDETPI 120  
DB 61 rkscrnpdpvngvhwikigiofsgsqikyscctkgyrllgssatcitsgdtviwneetpi 120  
  
QY 121 CDRIPCGLPPTIANGDFTSISREYFHGVSVTYHCNLSGRGKVFELVGEPSITCTSKDD 180  
DB 121 cdripcglpptiangdftsisisreyfhgvsvtyhcnlsgrgkvfelvgepsitctskdd 180  
  
QY 181 QVGIMSGPAPQCIIPNK 197  
DB 181 qvgiwsgapqciipnk 197  
  
RESULT 3  
W75993 W75993 standard; Protein; 211 AA.  
XX  
AC W75993;  
XX  
XX

DT 18-JAN-1999 (first entry)  
 XX  
 DE Complement receptor type 1-like polypeptide CW7rgdcys.  
 XX  
 KW Complement receptor type-1; CRI; CM7; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9839433-A1.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PD 05-MAR-1998; 98WO-GB00727.  
 XX  
 PF 05-MAR-1997; 97GB-0004519.  
 XX  
 PR (ADPR-) ADPROTECH PLC.  
 XX  
 PA Cox VF, Mossakowska DEI, Smith RAG;  
 XX  
 PI WPI; 1998-506358/43.  
 XX  
 DR Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PI used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 XX  
 PS Claim 19; Page 57; 67pp; English.  
 XX  
 XX This is the amino acid sequence of CM7rgdcys, a protein that  
 CC consists of the short consensus repeats (SCR) 1 and 2 from the  
 CC complement receptor type 1 (CRI) fused to the SCR3 of CRI-like  
 CC protein (see W79236), and additionally having a C-terminal RGD  
 CC sequence as a ligand for the glycoprotein IIb/IIIa of platelets.  
 CC CM7rgdcys was expressed in Escherichia coli from plasmid  
 CC pBroSCRI-3CM7rgdcys. The invention provides novel soluble  
 CC CRI derivatives (see W79236-47 and W75986-94) that act as  
 CC complement inhibitors with functional complement inhibitory,  
 CC including anti-haemolytic, activity. These can be used to treat a  
 CC disease or disorder associated with inflammation or inappropriate  
 CC complement activation, such as neurological disorders (e.g.  
 CC multiple sclerosis and Parkinson's disease), disorders of  
 CC inappropriate or undesirable complement activation (e.g. xenograft  
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,  
 CC infection or sepsis, immune complex reperfusion conditions,  
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and  
 CC myasthenia gravis), and reproductive disorders.  
 CC  
 XX  
 SO Sequence 211 AA:

Query Match 100.0%; Score 1104; DB 19; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-99;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOCNAPBMLFAPRTNLTDEFFPIGYLYNECPGSGRPFSTICLKNSVWTGAKDRCR 60  
 Db 1 mqcnawepmlfaprtnltdelfipiglylyneccpgysgrpfsticlknsvwtgakdr 60

QY 61 RKSCRNPPDVGNGVAVHVKIGIOFGSQIKYSCTKGRLIGSSASACIISGDPVIMDNTEPI 120  
 Db 61 rkscrrppdvgngvavhvkigifsgqikysctkyrlilgssasacilsgdtvawdnecpl 120

QY 121 CDRIPGCLPPTIANGDFTSISREYFHGSVVYTHCNLGSRRKVFELVGPESIVCTSKRD 180  
 Db 121 cdrilpgclppltiangdftsistreyfhgsvvlythcnlgsrgkxvfelvgpsivctskdd 180

QY 181 QVGIWSPAPQCITIPNK 197  
 Db 181 qvgiwsqapqcitipnk 197

RESULT 4  
 W75994  
 ID W75994 standard; Protein; 214 AA.  
 XX  
 AC W75994;  
 XX  
 DT 18-JAN-1999 (first entry)  
 XX  
 DE Complement receptor type 1-like polypeptide CM7/Tcell.  
 XX  
 KW Complement receptor type-1; CRI; CM7/Tcell; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9839433-A1.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PD 05-MAR-1998; 98WO-GB00727.  
 XX  
 PF 05-MAR-1997; 97GB-0004519.  
 XX  
 PR (ADPR-) ADPROTECH PLC.  
 XX  
 PA Cox VF, Mossakowska DEI, Smith RAG;  
 XX  
 PI WPI; 1998-506358/43.  
 XX  
 DR Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PI used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 XX  
 PS Claim 19; Page 58; 67pp; English.  
 XX  
 XX This is the amino acid sequence of CM7/Tcell, a protein that  
 CC consists of the short consensus repeats (SCR) 1 and 2 from the  
 CC complement receptor type 1 (CRI) fused to the SCR3 of CRI-like  
 CC protein (see W79236), and additionally having a C-terminal  
 CC extension that targets the protein to the T-cell receptor alpha  
 CC subunit. CM7/Tcell was expressed in Escherichia coli from plasmid  
 CC pBroSCRI-3CM7/Tcell. The invention provides novel soluble  
 CC CRI derivatives (see W79236-47 and W75986-94) that act as  
 CC complement inhibitors with functional complement inhibitory,  
 CC including anti-haemolytic, activity. These can be used to treat a  
 CC disease or disorder associated with inflammation or inappropriate  
 CC complement activation, such as neurological disorders (e.g.  
 CC multiple sclerosis and Parkinson's disease), disorders of  
 CC inappropriate or undesirable complement activation (e.g. xenograft  
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,  
 CC and acute pancreatitis), post-ischaemic reperfusion conditions,  
 CC infection or sepsis, immune complex disorders and autoimmune  
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and  
 CC myasthenia gravis), and reproductive disorders.  
 CC  
 XX  
 SO Sequence 214 AA:

Query Match 100.0%; Score 1104; DB 19; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-99;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOCNAPBMLFAPRTNLTDEFFPIGYLYNECPGSGRPFSTICLKNSVWTGAKDRCR 60

```

Db      1  mgnapewlpfarpnltdfefipgtlylncerpysgrpfslclksnwtgkdrct 60
QY      61  RKSCHNPPDPVNGMWHVIGIQFGSOIKRISCTKGYRLIGSSATCIISGDTVIMDNETPI 120
Db      61  Rkschnpdpvngmwhvixgqifgsgqikysctkgyrligssatcclisgdtvwdnetpl 120
QY      121  CDRIPCGLPPTIANGDFTSISREYFHGVSVMYHCLGSRGKVFELVGEPSIYCTSKDD 180
Db      121  cdripcglpptiangdftsistreyfhgsvvlyhcnlgsgkrfelvgpslyctskdd 180
QY      181  QVGIMSGAPQCIIPNK 197
Db      181  gvgiwsqpapqcilpnk 197

RESULT  5
W75987  ID      W75987 standard; Protein; 215 AA.
AC      W75987;
DE      18-JAN-1999 (first entry)
XX
DE      Complement receptor type 1-like polypeptide PM-9.
XX
KW      Complement receptor type-1; CRI; CM7; PM-9; complement; inhibitor;
KW      myristoyl/electrostatic switch peptide reagent 1; MSMP-1;
KW      anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW      xenograft rejection; inflammation; Crohn's disease; asthma;
KW      pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW      autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW      myasthenia gravis; reproductive disorder; therapy.
XX
OS      Chimeric - Homo sapiens.
XX
FH      Key
FH      Protein
FH      Location/Qualifiers
FT      1..197
FT      /label= CM7
FT      Peptide
FT      199..215
FT      /label= MSMP-1
FT      Disulfide-bond
FT      198..199
FT      Modified-site
FT      199
FT      /note= "(S-2-thiopyridyl)cysteine"
FT      Modified-site
FT      215
FT      /note= "N-(myristoyl)-glycine"
XX
PN      WO9839433-A1.
XX
PD      11-SEP-1998.
XX
PF      05-MAR-1998; 98WO-GB00727.
XX
PR      05-MAR-1997; 97GB-0004519.
XX
PA      (ADPR-) ADPROTECH PLC.
XX
PI      Cox VF, Mossakowska DEI, Smith RAG;
XX
DR      WPI; 1998-506358/43.
XX
PT      Soluble polypeptide comprising short consensus repeats from LHR-A -
PT      used to treat disorders and diseases associated with inflammation or
PT      inappropriate complement activation
XX
PS      Claim 17: Page 52-53; 67pp; English.
XX
CC      This is the amino acid sequence of PM-1, or (CM7)-Cys-S-S-(MSMP-1),
CC      comprising novel soluble complement receptor type 1 (CRI)-like
CC      polypeptide CM7 (see W79236) joined to a myristoyl/electrostatic
CC      switch peptide reagent 1 (MSMP-1). It was produced by coupling
CC      CM7/Cys (see W75986) to a synthetic MSMP-1 peptide. CM7 comprises

```

```

CC      the short consensus repeats (SCR) 1 and 2 from CRI and SCR3 of the
CC      CRI-like protein (see W79247). Soluble CRI-derived proteins of the
CC      invention (see W53236-47 and W75987-94) act as complement inhibitors
CC      with functional complement inhibitory, including anti-hemolytic,
CC      activity. These can be used to treat a disease or disorder
CC      associated with inflammation or inappropriate complement activation,
CC      such as neurological disorders (e.g. multiple sclerosis, Parkinson's
CC      disease), disorders of inappropriate or undesirable complement
CC      activation (e.g. xenograft rejection), inflammatory disorders (e.g.
CC      Crohn's disease, asthma, and acute pancreatitis), post-ischaemic
CC      reperfusion conditions, infection or sepsis, immune complex
CC      disorders and autoimmune diseases (e.g. rheumatoid arthritis,
CC      proliferative nephritis and myasthenia gravis), and reproductive
CC      disorders.
XX
SQ      Sequence 215 AA;

Query Match      100.0%; Score 1104; DB 19; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MQCNAPEWLPPARPNTLDEFEFPAGTYLNECRGSGRPFSTICLKNVWTGAKRCR 60
Db      1  mgnapewlpfarpnltdfefipgtlylncerpysgrpfslclksnwtgkdrct 60
QY      61  RKSCHNPPDPVNGMWHVIGIQFGSOIKRISCTKGYRLIGSSATCIISGDTVIMDNETPI 120
Db      61  Rkschnpdpvngmwhvixgqifgsgqikysctkgyrligssatcclisgdtvwdnetpl 120
QY      121  CDRIPCGLPPTIANGDFTSISREYFHGVSVMYHCLGSRGKVFELVGEPSIYCTSKDD 180
Db      121  cdripcglpptiangdftsistreyfhgsvvlyhcnlgsgkrfelvgpslyctskdd 180
QY      181  QVGIMSGAPQCIIPNK 197
Db      181  gvgiwsqpapqcilpnk 197

RESULT  6
W79240  ID      W79240 standard; Protein; 197 AA.
AC      W79240;
DE      18-JAN-1999 (first entry)
XX
DE      Complement receptor type 1-like protein CM5.
XX
KW      Complement receptor type-1; CRI; CM5; complement; inhibitor;
KW      anti-haemolytic; multiple sclerosis; Parkinson's disease;
KW      xenograft rejection; inflammation; Crohn's disease; asthma;
KW      pancreatitis; post-ischaemic reperfusion; infection; sepsis;
KW      autoimmune disease; rheumatoid arthritis; proliferative nephritis;
KW      myasthenia gravis; reproductive disorder; therapy.
XX
OS      Homo sapiens.
XX
FH      Synthetic.
XX
PN      WO9839433-A1.
XX
PD      11-SEP-1998.
XX
PF      05-MAR-1998; 98WO-GB00727.
XX
PR      05-MAR-1997; 97GB-0004519.
XX
PA      (ADPR-) ADPROTECH PLC.
XX
PI      Cox VF, Mossakowska DEI, Smith RAG;
XX
DR      WPI; 1998-506358/43.
XX
DR      N-PSDB; V53272.

```

Query Match	97.6%	Score 1077	DB 19	Length 197		
Best Local Similarity	97.5%	Pred. No. 9.9e-97				
Matches 192	Conservative 1	Mismatches 4	Indels 0	Gaps 0		
QY 1	MQCNAPMLPFA	RPTNLIDEE	FEFPIGTYL	INTECRPGYSGRPF	SIICLNKNSVTGAKR	CR 60
Db 1	mqcnapewlpf	arpnliddef	ifpigtlyl	nyecrpgysrps	isiclnksvgtgkdr	cr 60
QY 61	RKSCNPPDPV	NGMHVYIK	GIOFSQIK	YSCSKGRRLIG	SSSATTICISD	TYIMNEPI 120
Db 61	rkschnpdpv	ngmhwvlyk	gigsqlysc	tkxyrlligsssa	atcllsgdtyl	iwnepepi 120
QY 121	CDRIICGAPPT	ANGDFTS	IREHYG	SVVYHGNL	SGRGKVELV	GEPSIYCTSKRD 180
Db 121	cdriicgapp	pttltngd	ftstrenf	hygsavtyh	cnlsgrgkvel	lvgepsiyctskd 180
QY 181	QVGIWSPAP	QCIIPNK	197			
Db 181	qvgiws	papqcllpnk	197			
RESULT 8						
ID W79237	standard	Protein	197 AA			

AC W79237;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Complement receptor type 1-like protein CMI.  
XX  
KW Complement receptor type-1; CRI; CMI; complement; inhibitor;  
KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
KW xenograft rejection; inflammation; Crohn's disease; asthma;  
KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
KW myasthenia gravis; reproductive disorder; therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN MO9839433-A1.  
XX  
PD 11-SEP-1998.  
XX  
PE 05-MAR-1998; 98WO-GB00727.  
XX  
PR 05-MAR-1997; 97GB-0004519.  
XX  
PA (ADPR-) ADPROTECH PLC.  
XX  
PI Cox VF, Mossakowska DEI, Smith RAG;  
XX  
DR WPI: 1998-506358/43.  
DR N-PSDB: V53269.  
XX  
PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
PT used to treat disorders and diseases associated with inflammation or  
PT inappropriate complement activation  
XX  
PS Claim 13; Page 44; 67pp; English.  
XX  
CC This is the amino acid sequence of CMI, a protein that consists  
CC of the short consensus repeats (SCR) 1 and 2 from complement  
CC receptor type 1 (CRI) fused to an SCR3 (see W79242) in which 5 amino  
CC acids were altered to those found in the SCR3 of the encoded protein  
CC of the CRI-like pseudogene (cripse). CMI DNA (see V53269) was  
CC constructed by site-directed mutagenesis (see V53263) of plasmid  
CC pBI013-5, which codes for SCR1-3 of CRI. pBROCCRI-3CMI carrying  
CC CMI DNA was used to transform Escherichia coli BL21(DE3), and CMI  
CC was purified from solubilised inclusion bodies. The invention  
CC provides DNA sequences (see V53262 and V53269-79) encoding novel  
CC soluble engineered CRI polypeptides (see W53236-47) such as CMI  
CC that act as complement inhibitors with functional complement  
CC inhibitory, including anti-haemolytic, activity. These can be used  
CC to treat a disease or disorder associated with inflammation or  
CC inappropriate complement activation, such as neurological disorders  
CC (e.g. multiple sclerosis and Parkinson's disease), disorders of  
CC inappropriate or undesirable complement activation (e.g. xenograft  
CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,  
CC and acute pancreatitis), post-ischaemic reperfusion conditions,  
CC infection or sepsis, immune complex disorders and autoimmune  
CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and  
CC myasthenia gravis), and reproductive disorders.  
XX  
SQ Sequence 197 AA;  
Query Match 97.3%; Score 1074; DB 19; Length 197;  
Best Local Similarity 97.5%; Pred. No. 1.9e-96;  
Matches 192; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MOCNAPENLPPARPNTLDEEFFPIGTYLNTCEPARGSGRPFSSICLNKSNVTGAKDCR 60  
Db 1 mqcnapewlparpnntldedefpigtlylntceprgysgrpfssiclnkswtgskdcr 60  
OY 61 RKSGRNPDPVNGKWHVKGIOFGSOIYSCTKGRLIGSSAGTCIIGDVIYDNEPTPI 120  
|||||

Db 61 rksgrnpdpvngkwhvkgiofgsqikysctkgryllgssatcilsqgdvtdwnepti 120  
OY 121 CDRTPCGLPPIIANGDFISRETFHYSVVTYHCNCLSGRKKYFELVGEPSIYCTSKD 180  
|||||  
Db 121 cdripcgipgliangdfitsireyfhysvvtlycnpbgsggrkfyelvgepslyctsnd 180  
OY 181 QVGISGAPQCIIIPNK 197  
Db 181 qvgilwsgpapgcllpnk 197  
RESULT 9  
W79238  
ID W79238 standard; Protein; 197 AA.  
XX  
AC W79238;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Complement receptor type 1-like protein CM2.  
XX  
KW Complement receptor type-1; CRI; CM2; complement; inhibitor;  
KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
KW xenograft rejection; inflammation; Crohn's disease; asthma;  
KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
KW myasthenia gravis; reproductive disorder; therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN MO9839433-A1.  
XX  
PD 11-SEP-1998.  
XX  
PE 05-MAR-1998; 98WO-GB00727.  
XX  
PR 05-MAR-1997; 97GB-0004519.  
XX  
PA (ADPR-) ADPROTECH PLC.  
XX  
PI Cox VF, Mossakowska DEI, Smith RAG;  
XX  
DR WPI: 1998-506358/43.  
DR N-PSDB: V53270.  
XX  
PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
PT used to treat disorders and diseases associated with inflammation or  
PT inappropriate complement activation  
XX  
PS Claim 13; Page 44-45; 67pp; English.  
XX  
CC This is the amino acid sequence of CM2, a protein that consists  
CC of the short consensus repeats (SCR) 1 and 2 from complement  
CC receptor type 1 (CRI) fused to an SCR3 (see W79243) in which 4 amino  
CC acids were altered to those found in the SCR3 of the encoded protein  
CC of the CRI-like pseudogene (cripse). CM2 DNA (see V53270) was  
CC constructed by site-directed mutagenesis (see V53264) of plasmid  
CC pBI013-5, which codes for SCR1-3 of CRI. pBROCCRI-3CM2 carrying  
CC CM2 DNA was used to transform Escherichia coli BL21(DE3), and CM2  
CC was purified from solubilised inclusion bodies. The invention  
CC provides DNA sequences (see V53262 and V53269-79) encoding novel  
CC soluble engineered CRI polypeptides (see W53236-47) such as CM2  
CC that act as complement inhibitors with functional complement  
CC inhibitory, including anti-haemolytic, activity. These can be used  
CC to treat a disease or disorder associated with inflammation or  
CC inappropriate complement activation, such as neurological disorders  
CC (e.g. multiple sclerosis and Parkinson's disease), disorders of  
CC inappropriate or undesirable complement activation (e.g. xenograft  
CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,  
CC and acute pancreatitis), post-ischaemic reperfusion conditions,  
CC infection or sepsis, immune complex disorders and autoimmune  
CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and



CC myasthenia gravis), and reproductive disorders.  
 XX Sequence 197 AA:  
 SQ

Query Match 97.1%; Score 1072; DB 19; Length 197;  
 Best Local Similarity 97.0%; Pred. No. 3e-96;  
 Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MOCNAPEMLPFARPTNLNDEFEFPIGTIYNTYECRPGYSGRPSIICLKNSWTGAKDR 60  
 DB 1 mcgnapewlpfarpnltdfeipigtlylneecrpgysgrpfisiclknswtgaktddr 60  
 QY 61 RSCSNPDPVNGMWHVIRIGIQFGSQIKKSCYKGRYLIISSATCIIISGDTYIMDNETPI 120  
 DB 61 rscsnppdpvngmwhvirigifgsgikysckgyrllyssatcclisgdtvymdnecp1 120  
 QY 121 CDRIPCGLPPTIANGDFTSISREYFHYGSVVTYHGNLGRGKKVPELVGEPSTYCTSKD 180  
 DB 121 cdrpcglppltingdftstrenenfhygsvtvtyhcnlgsgkfkvelvgepslyctsknd 180  
 QY 181 QVIGMSGAPQCIIPNK 197  
 DB 181 qvlgwsgpapgcllppnk 197

RESULT 10  
 ID W79239 standard; Protein: 197 AA.  
 AC W79239;

DT 18-JAN-1999 (first entry)  
 DE Complement receptor type 1-like protein CM3.

XX Complement receptor type-1; CRI; CM3; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy.

OS Homo sapiens.  
 OS Synthetic.

PN WO9839433-A1.

PD 11-SEP-1998.

PF 05-MAR-1998; 98WO-GB00727.

PR 05-MAR-1997; 97GB-0004519.

PA (ADPR-) ADPROTECH PLC.

PI Cox VF, Mossakowska DEL, Smith RAG;

DR WPI: 1998-506358/43.

DR N-PSDB: V53271.

PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PI used to treat disorders and diseases associated with inflammation or  
 PI inappropriate complement activation

XX Claim 13; Page 45-46; 67pp; English.

CC This is the amino acid sequence of CM3, a protein that consists  
 CC of the short consensus repeats (SCR) 1 and 2 from complement  
 CC receptor type 1 (CRI) fused to an SCR3 (see W79244) in which 1 amino  
 CC acid was altered to that found in the SCR3 of the encoded protein  
 CC of the CRI-like pseudogene (Cripse). CM3 DNA (see V53271) was  
 CC constructed by site-directed mutagenesis (see V53265) of plasmid

CC PDB1013-5, which codes for SCR1-3 of CRI. pBROSCRI-3CM3 carrying  
 CC CM3 DNA was used to transform Escherichia coli BL21(DE3), and CM3  
 CC was purified from solubilised inclusion bodies. The invention  
 CC provides DNA sequences (see V53262 and V53269-79) encoding novel  
 CC soluble engineered CRI polypeptides (see W53236-47) such as CM3  
 CC that act as complement inhibitors with functional complement  
 CC inhibitory, including anti-haemolytic, activity. These can be used  
 CC to treat a disease or disorder associated with inflammation or  
 CC inappropriate complement activation, such as neurological disorders  
 CC (e.g. multiple sclerosis and Parkinson's disease), disorders of  
 CC inappropriate or undesirable complement activation (e.g. xenograft  
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,  
 CC and acute pancreatitis), post-ischaemic reperfusion conditions,  
 CC infection or sepsis, immune complex disorders and autoimmune  
 CC diseases (e.g. rheumatoid arthritis, proliferative nephritis and  
 CC myasthenia gravis), and reproductive disorders.

SO Sequence 197 AA:

Query Match 95.3%; Score 1052; DB 19; Length 197;  
 Best Local Similarity 95.4%; Pred. No. 2.6e-94;  
 Matches 188; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MOCNAPEMLPFARPTNLNDEFEFPIGTIYNTYECRPGYSGRPSIICLKNSWTGAKDR 60  
 DB 1 mcgnapewlpfarpnltdfeipigtlylneecrpgysgrpfisiclknswtgaktddr 60  
 QY 61 RSCSNPDPVNGMWHVIRIGIQFGSQIKKSCYKGRYLIISSATCIIISGDTYIMDNETPI 120  
 DB 61 rscsnppdpvngmwhvirigifgsgikysckgyrllyssatcclisgdtvymdnecp1 120  
 QY 121 CDRIPCGLPPTIANGDFTSISREYFHYGSVVTYHGNLGRGKKVPELVGEPSTYCTSKD 180  
 DB 121 cdrpcglppltingdftstrenenfhygsvtvtyhcnlgsgkfkvelvgepslyctsknd 180  
 QY 181 QVIGMSGAPQCIIPNK 197  
 DB 181 qvlgwsgpapgcllppnk 197

RESULT 11  
 ID W75991 standard; Protein: 198 AA.

AC W75991;

DT 18-JAN-1999 (first entry)

DE Complement receptor type 1-like polypeptide CM16/cys.

XX Complement receptor type-1; CRI; CM16; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy.

OS Homo sapiens.  
 OS Synthetic.

PN WO9839433-A1.

PD 11-SEP-1998.

PF 05-MAR-1998; 98WO-GB00727.

PR 05-MAR-1997; 97GB-0004519.

PA (ADPR-) ADPROTECH PLC.

PI Cox VF, Mossakowska DEL, Smith RAG;

DR WPI; 1998-506358/43.  
 XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PT used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 XX  
 PS Claim 19; Page 55-56; 67pp; English.  
 XX  
 CC This is the amino acid sequence of CM16/cys5, a protein derived  
 CC from CM15/cys (see W75989) with the modification I124P (1.e.  
 CC wild-type sequence at the hinge region between SCR2 and SCR3).  
 CC CM15/cys consists of the short consensus repeats (SCR) 1-3 of the  
 CC complement receptor type 1 (CRI) in which 23 amino acids have been  
 CC substituted by those found at homologous positions of the CRI-like  
 CC pseudogene sequence, plus an additional C-terminal cysteine residue.  
 CC CM16/cys was expressed from plasmid pROSCRI-3CM16/cys in  
 CC Escherichia coli, and was used in the construction of  
 CC (CM16)-Cys-S-S-(MSWP-1) (see W75992). The invention provides novel  
 CC soluble CRI-derived polypeptides (see W5336-47 and W75986-94) that  
 CC act as complement inhibitors with functional complement inhibitory,  
 CC including anti-haemolytic, activity. They are used to treat a  
 CC disease or disorder associated with inflammation or inappropriate  
 CC complement activation, such as neurological disorders (e.g.  
 CC multiple sclerosis and Parkinson's disease), disorders of  
 CC inappropriate or undesirable complement activation (e.g. xenograft  
 CC rejection), inflammatory disorders (e.g. Crohn's disease, asthma,  
 CC infection or sepsis, immune complex disorders and autoimmune  
 CC diseases (e.g. rheumatoid arthritis), proliferative nephritis and  
 CC myasthenia gravis), and reproductive disorders.  
 CC  
 XX Sequence 198 AA;  
 XX  
 QY Query Match 95.1%; Score 1050; DB 19; Length 198;  
 XX Best Local Similarity 93.9%; Pred. No. 4.1e-94;  
 XX Matches 185; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 XX  
 QY 1 MGNAPEMLEFARPTNLTDEFEPIGTLYNIECRPGYSGRPESITCLKNSWTGANDRCR 60  
 XX |||||  
 DB 1 mgnvpewlpfarpnltdldfelfpigtlynyeocpysgpfslclknswtsakck 60  
 XX  
 QY 61 RKSCRNPDPVNGVMVAVIKIQGSGIKYSCITKGYRLIGSSSACITISGDTYVINDETPI 120  
 XX |||||  
 DB 61 rkscrnpdpvngvmavikidqfsgikyscpkyrligssatcilsnltvldnktpr 120  
 XX  
 QY 121 CDRIPGGLPPTINGDFTSISREFFHGSVVTYHCNLSGSKKVFELVGEPSITCTSKD 180  
 XX |||||  
 DB 121 cdripcgllpplangdftsrsrefffhgsvvtynhcnlsgskvfkelfvgepsitctskd 180  
 XX  
 QY 181 QVGIWSGPAPQCITIPNK 197  
 XX |||||  
 DB 181 qvgiwsqapapqciltipnk 197  
 XX  
 RESULT 12  
 ID W75992  
 XX W75992 standard; Protein: 215 AA.  
 AC W75992;  
 XX  
 DT 18-JAN-1999 (first entry)  
 XX  
 DE (CM16)-Cys-S-S-(MSWP-1) polypeptide.  
 XX  
 KW Complement receptor type-1; CRI; CM16; complement; inhibitor;  
 KW myristoyl/electrostatic switch peptide reagent 1; MSWP-1;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy.  
 XX

OS Chimeric - Homo sapiens.  
 OS Chimeric - Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 1..198  
 FT Peptide /label= CM16/cys  
 FT 199..215  
 FT Disulfide-bond /label= MSWP-1  
 FT Modified-site 199  
 FT Modified-site /note= "(S-2-thioglycidyl)cysteine"  
 FT Modified-site /note= "N-(myristoyl)-glycine"  
 XX  
 PN W09839433-A1.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PF 05-MAR-1998; 98WO-GB00727.  
 XX  
 PR 05-MAR-1997; 97GB-0004519.  
 XX  
 PA (ADPR-) ADPROTECH PLC.  
 XX  
 PI Cox VF, Mossakowska DEL, Smith RMG;  
 XX  
 DR WPI; 1998-506358/43.  
 XX  
 XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PT used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 XX  
 PS Claim 17; Page 56; 67pp; English.  
 XX  
 CC This is the amino acid sequence of (CM16)-Cys-S-S-(MSWP-1),  
 CC comprising novel soluble complement receptor type 1 (CRI)-like  
 CC polypeptide CM16 joined to a myristoyl/electrostatic switch peptide  
 CC reagent 1 (MSWP-1). It was produced by coupling CM16/cys (see  
 CC W75989) to a synthetic MSWP-1 peptide (see W53988). CM16 comprises  
 CC the short consensus repeats (SCR) from CRI in which 23 amino acid  
 CC residues are substituted by those corresponding to the CRI-like  
 CC pseudogene. Soluble CRI-derived polypeptides of the invention (see  
 CC W53236-47 and W75987-94) act as complement inhibitors with  
 CC functional complement inhibitory, including anti-hemolytic,  
 CC activity. These can be used to treat a disease or disorder  
 CC associated with inflammation or inappropriate complement activation,  
 CC such as neurological disorders (e.g. multiple sclerosis, Parkinson's  
 CC disease), disorders of inappropriate or undesirable complement  
 CC activation (e.g. xenograft rejection), inflammatory disorders (e.g.  
 CC Crohn's disease, asthma, and acute pancreatitis), post-ischaemic  
 CC reperfusion conditions, infection or sepsis, immune complex  
 CC disorders and autoimmune diseases (e.g. rheumatoid arthritis,  
 CC proliferative nephritis and myasthenia gravis), and reproductive  
 CC disorders.  
 CC  
 XX Sequence 215 AA;  
 XX  
 QY Query Match 95.1%; Score 1050; DB 19; Length 215;  
 XX Best Local Similarity 93.9%; Pred. No. 4.5e-94;  
 XX Matches 185; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 XX  
 QY 1 MGNAPEMLEFARPTNLTDEFEPIGTLYNIECRPGYSGRPESITCLKNSWTGANDRCR 60  
 XX |||||  
 DB 1 mgnvpewlpfarpnltdldfelfpigtlynyeocpysgpfslclknswtsakck 60  
 XX  
 QY 61 RKSCRNPDPVNGVMVAVIKIQGSGIKYSCITKGYRLIGSSSACITISGDTYVINDETPI 120  
 XX |||||  
 DB 61 rkscrnpdpvngvmavikidqfsgikyscpkyrligssatcilsnltvldnktpr 120  
 XX  
 QY 121 CDRIPGGLPPTINGDFTSISREFFHGSVVTYHCNLSGSKKVFELVGEPSITCTSKD 180  
 XX |||||  
 DB 121 cdripcgllpplangdftsrsrefffhgsvvtynhcnlsgskvfkelfvgepsitctskd 180  
 XX

QY 181 OVGISGAPACIIPNK 197  
 Db 181 qvgIwsgpqpcllpnk 197

## RESULT 13

R47152  
 ID R47152 standard: protein; 197 AA.

AC R47152;

DT 18-JUL-1994 (first entry)

DE Sequence of soluble complement receptor type 1 (CRI) derivative  
 DE which comprises the N-terminal fragment MQ1-K196 of CRI.

KM Complement receptor type 1; CRI; short consensus repeat;

KW Long homologous repeat; domain; inflammation; therapy.

OS Synthetic.

PN WO9400571-A.

PD 06-JAN-1994.

PF 16-JUN-1993; 93WO-GB01282.

PR 24-JUN-1992; 92GB-0013376.

PR 01-MAR-1993; 93GB-0004057.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Dodd I, Freeman AM, Mossakowska DEI, Smith RAG;

WPI; 1994-026208/03.

PT New soluble complement receptor type 1 derivs. - used for  
 PT treating disease or disorder associated with inflammation or  
 PT inappropriate complement activation

PS Claim 13: Page 49-50; 65pp; English.

CC CRI is composed of 30 short consensus repeats (SCRs) that each  
 CC contain around 60-70 AAs. It is further arranged as 4 long  
 CC homologous repeats (LHRs) of 7 SCRs each. Following a leader  
 CC sequence, the CRI molecule consists of the N-terminal LHR-A, the  
 CC next two repeats, LHR-B and LHR-C, and the most C-terminal LHR-D,  
 CC followed by 2 additional SCRs, a 25 residue putative transmembrane  
 CC region and a 43 residue cytoplasmic tail. Based on the mature CRI  
 CC molecule, having a predicted N-terminal Glu, designated residue 1,  
 CC the first four SCR domains of LHR-A are 2-58, 63-120, 125-191 and  
 CC 197-552, of mature CRI. Soluble fragments of CRI which corresp. to  
 CC part of CRI possess functional complement inhibitory, including  
 CC anti-haemolytic, activity.

CC Sequence 197 AA;

QY Query Match 94.8%; Score 1047; DB 15; Length 197;

Best Local Similarity 94.9%; Pred. No. 7, 9e-94;

Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MOCNAPFMDLPARPTNTDEFEPIGYLNECRPGYSGRPFSITCKNSVMTGAKDRCR 60

Db 1 mcgnapwlpfarpntldefefpigtlylneecrpgysgrpfslcklnsvwtgaktcr 60

QY 61 RKSRCNPDVPMGVNHYIKGQFSGQIKYSCTRKRYRLIGSSATCIISGDTVINDNETPI 120

Db 61 rkscrpdpvpmgvnmhvikgqfsgqikysctkryrligssatciisgdtvindnetpi 120

QY 121 CDRIPGCLPTPIANGDFTSISREYFHGVSVYTYHCNLSRCKKVFELVGEISIVCTSKDD 180

Db 121 cdrpfcglptpiangdftsisreafhvgsvvtytyhcnlsrckkvvfelvgeisivctskdd 180  
 QY 181 OVGISGAPACIIPNK 197  
 Db 181 qvgIwsgpqpcllpnk 197

## RESULT 14

W45897  
 ID W45897 standard: peptide; 198 AA.

AC W45897;

DT 30-JUN-1998 (first entry)

DE SCR 1-3 of complement receptor type 1 (CRI).

KM Membrane binding element; thrombotic disease; soluble protein;

KW complement-related disease; integral membrane protein; inflammation;

KM short consensus repeat; SCR 1-3; CRI; complement receptor type 1.

OS Homo sapiens.

PN Key

PD Cross-links

PF 198

FT /note- "Disulphide linked to Cys in peptide given

FT in W45889, W45892, W45893 or W45894"

PN WO9802454-A2.

PD 22-JAN-1998.

PF 08-JUL-1997; 97WO-EP03715.

PR 15-JUL-1996; 96GB-0014871.

PA (ADPR-) ADPROTECH PLC.

PI Dodd I, Mossakowska DEI, Smith RAG;

WPI; 1998-110524/10.

PT Derivatives of soluble poly(peptide)s bonded to low affinity

PT membrane binding groups - useful for treating complement-related and

PT thrombotic diseases, providing improved localisation at cellular

PT membranes

PS Claim 22: Page 59; 75pp; English.

CC This sequence represents a specifically claimed protein having the  
 CC amino acid sequence of short consensus repeats (SCR 1-3) of  
 CC complement receptor type (1CRI) plus a single terminal Cys. The  
 CC invention relates to a soluble derivative (A) of a soluble polypeptide  
 CC (1), which comprises at least 2 heterologous membrane-binding elements  
 CC (MBE) of low membrane affinity covalently associated with (1). MBE  
 CC interact, independently and with thermodynamic additivity, with  
 CC components of cellular or artificial membranes exposed to extracellular  
 CC fluids. (A) are used to treat disorders treatable with (1) itself,  
 CC specifically inflammation or any other complement-related disorder  
 CC (e.g. neurological disease, graft rejection, myocardial infarction,  
 CC sepsis, rheumatoid arthritis and many others; including application to  
 CC indwelling devices) and thrombolytic disease, but also to treat allergy,  
 CC induce weight loss, to treat ischaemia or asthma and as immuno-  
 CC modulators for treating multiple sclerosis. (A) are administered orally,  
 CC topically, by injection or inhalation at 0.01-10 (preferably 0.1-10)  
 CC mg/kg/day.

CC Sequence 198 AA;

QY Query Match 94.8%; Score 1047; DB 19; Length 198;

Best Local Similarity 94.9%; Pred. No. 7, 9e-94;

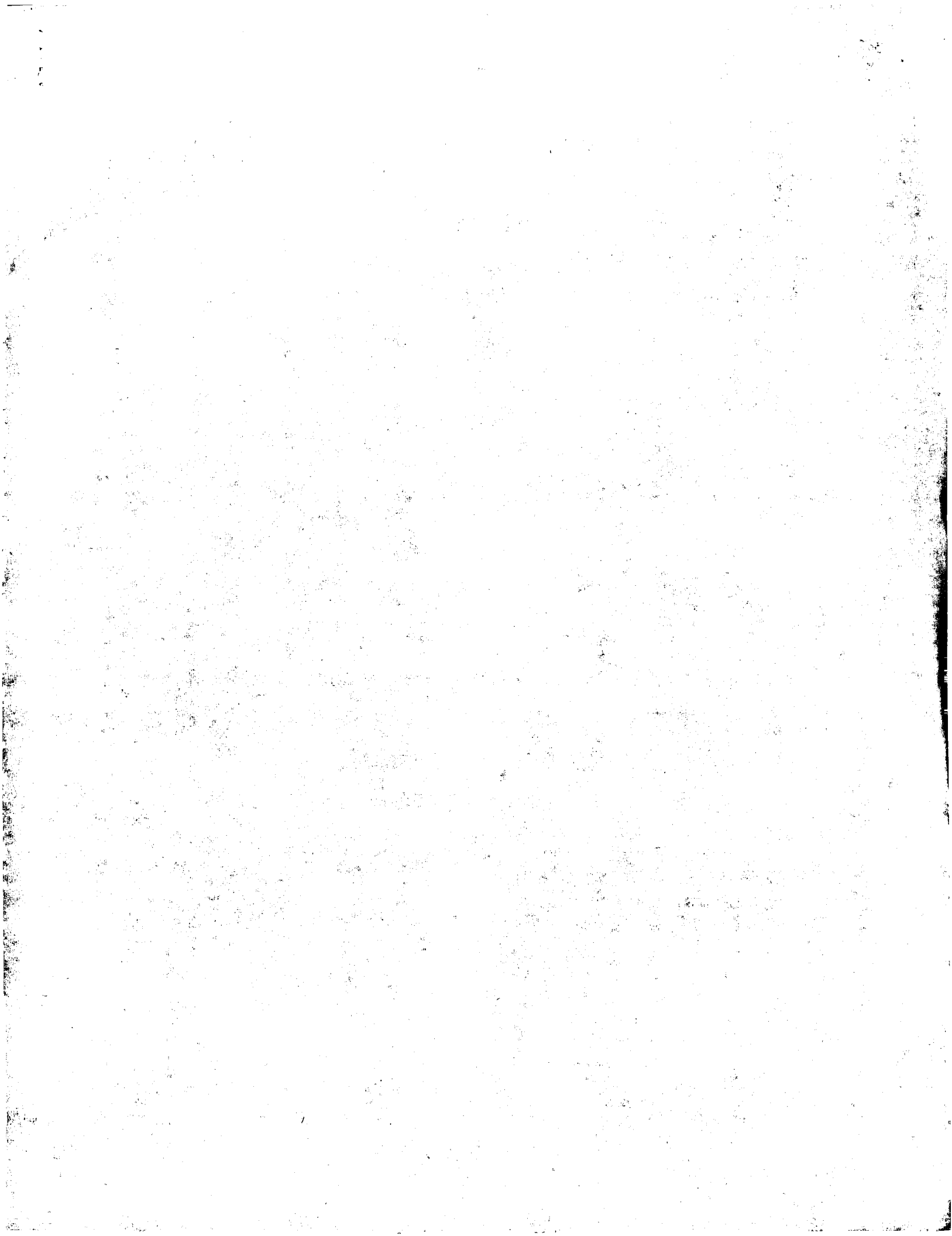
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY	1	MOGNAPFELPARPTNTLTDEEPIGIVYLXECRPGYSGPFSIIICLNKSVMTGARDRC	60
Db	1	mqcnapewlfparptnltdetefefbigyilyneecrpgysgrpfilclnksvwtgaktcr	60
QY	61	RKSCRNPDPVNGVAVHVIKGIQFSGQIKYKTSCTKGYRLIGSSNATCIISGDYIMDNERP	120
Db	61	rkscrnpdpvngvavhvikgigfsgqikysctkxyrligssatcillsgdvtvmdnetp	120
QY	121	CDRIIPCGIPRIANGDSTISREFFHGSVWYTHCNIGSGKKVFLVQEPSTYCSKSD	180
Db	121	cdriipcgiprltngdstisrenfhygsvwyrcmpsggkrxvflvqepstysctsnd	180
QY	181	QVGIMSGPAPQCIIIPNK 197	
Db	181	qvqimsgpapqciiipnk 197	
RESULT	15		
ID	W45909	W45909 standard; peptide; 211 AA.	
XX	AC	W45909;	
XX	DT	30-JUN-1998 (first entry)	
XX	DE	SCR 1-3 of complement receptor type 1 (CRI) derived protein.	
XX	KW	Membrane binding element; thrombotic disease; soluble protein;	
XX	KW	complement-related disease; integral membrane protein; inflammation;	
XX	KW	short consensus repeat; SCR 1-3; CRI; complement receptor type 1.	
XX	OS	Homo sapiens.	
XX	FM	Key	Location/Qualifiers
XX	FT	Cross-links	211
XX	FT	/note= "Disulphide linked to Cys in peptide given	
XX	FT	in W45889"	
XX	PN	W09802454-A2.	
XX	PD	22-JAN-1998.	
XX	PF	08-JUL-1997; 97WO-EP03715.	
XX	PR	15-JUL-1996; 96GB-0014871.	
XX	PA	(ADPR-) ADPROTECH PLC.	
XX	XX	Dodd I, Mossakowska DEI, Smith RAG;	
XX	PI	WPI: 1998-110524/10.	
XX	DR		
XX	PT	Derivatives of soluble poly:peptide(s) bonded to low affinity	
XX	PT	membrane binding groups - useful for treating complement-related	
XX	PT	chromobtic diseases, providing improved localisation at cellular	
XX	PT	membranes	
XX	PS	Claim 28; Page 65; 75pp; English.	
XX	CC	This sequence is shown in the specification. The invention relates to	
XX	CC	a soluble derivative (A) of a soluble polypeptide (1), which comprises	
XX	CC	at least 2 heterologous membrane-binding elements (MBE) of low membrane	
XX	CC	affinity covalently associated with (1). MBE interact, independently and	
XX	CC	with thermodynamic additivity, with components of cellular or artificial	
XX	CC	membranes exposed to extracellular fluids. (A) are used to treat	
XX	CC	disorders treatable with (1) itself, specifically inflammation or any	
XX	CC	other complement-related disorder (e.g. neurological disease, graft	
XX	CC	rejection, myocardial infarction, sepsis, rheumatoid arthritis and many	
XX	CC	others); including application to indwelling devices) and thrombolytic	
XX	CC	disease, but also to treat allergy, induce weight loss, to treat	
XX	CC	ischaemia or asthma and as immuno-modulators for treating multiple	
XX	CC	sclerosts. (A) are administered orally, topically, by injection or	

CC	Inhalation at 0.01-10 (preferably 0.1-10) mg/kg/day.									
XX										
SO	Sequence	211 AA;								
	Query Match	94.8%;	Score 1047;	DB 19;	Length 211;					
	Best Local Similarity	94.9%;	Pred. No. 8.6e-94;							
	Matches 187;	Conservative	2;	Mismatches 8;	Indels 0;	Gaps 0;				
QY	1	MCCANPEHLPPARPRINLDEFEFPICGTALYNECRPGYSGRPSSITCLKNSWTGAKDRCR	60							
Db	1	mqcnapewlpiatrpnlldetefpigtlylmyecrpgysgrfptstlclknswvtgaxdrcr	60							
QY	61	RKSCRNPPDPVNGMHWYIKGIQFQSQIKYSCSKGRIILGSSSATCIIISGDIYIMWNETPI	120							
Db	61	rksctnppdpvngmhwvlykglqfsgqlkysckkyrlllgssasatcllsgdtylwnepvl	120							
QY	121	CDRIPLCGILPPTIANDDEFISIKREYRHIGSVYTHCNLGSRKGVKVELVGEPSIYCTSKD	180							
Db	121	cdriplcglpplrltngdflstnrenahygsvvtlycmppsgsgrkvtelvgepsilyctsndd	180							
QY	181	OVGIMSGAPAOCLIPNK	197							
Db	181	qvgiwsppapgcilpnk	197							

Search completed: January 13, 2001, 13:42:31  
Job time: 3146 sec

---



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2001, 13:09:15 ; Search time 27.14 Seconds  
(without alignments)  
130.344 Million cell updates/sec

Title: US-09-380-682-1  
Perfect score: 1104  
Sequence: 1 MOCNAPWLPFARPNLTDE.....KDOVGWISGPAPQCIIPNK 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/Backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	94.8	197	2	US-08-356-361-27
2	1047	94.8	197	2	US-08-769-967A-27
3	1047	94.8	254	2	US-08-356-361-29
4	1047	94.8	254	2	US-08-356-361-30
5	1047	94.8	254	2	US-08-769-967A-29
6	1047	94.8	254	2	US-08-769-967A-30
7	1042	94.4	1847	5	5256642-10
8	1042	94.4	1847	5	5256642-10
9	1042	94.4	2039	5	5256642-2
10	1042	94.4	2039	5	5472939-2
11	788	71.4	1466	5	5256642-6
12	788	71.4	1466	5	5472939-6
13	788	71.4	1537	5	5256642-5
14	788	71.4	1537	5	5472939-5
15	408	37.0	323	1	US-08-435-149-2
16	408	37.0	324	1	US-08-310-416A-14
17	408	37.0	324	1	US-08-888-171-14
18	408	37.0	577	2	US-08-435-149-3
19	361	32.7	76	2	US-08-356-361-28
20	361	32.7	76	2	US-08-769-967A-28
21	361	32.7	133	2	US-08-356-361-31
22	361	32.7	133	2	US-08-769-967A-31
23	346	31.3	60	1	US-08-210-266A-10
24	346	31.3	60	1	US-08-688-675-10
25	346	31.3	60	3	US-08-477-860C-10
26	340	30.8	62	1	US-08-210-266A-12
27	340	30.8	62	1	US-08-688-675-12
28	340	30.8	62	3	US-08-477-860C-12

29	295	26.7	254	1	US-08-310-416A-13	Sequence 13, Appl
30	295	26.7	254	2	US-08-888-171-13	Sequence 13, Appl
31	295	26.7	254	2	US-08-435-149-1	Sequence 1, Appl1
32	295	26.7	293	1	US-08-310-416A-16	Sequence 16, Appl1
33	295	26.7	293	2	US-08-888-171-16	Sequence 16, Appl1
34	295	26.7	324	2	US-08-528-057-46	Sequence 46, Appl1
35	295	26.7	370	2	US-08-528-057-42	Sequence 42, Appl1
36	295	26.7	373	2	US-08-528-057-44	Sequence 44, Appl1
37	295	26.7	377	2	US-08-528-057-2	Sequence 2, Appl1
38	295	26.7	384	5	5514787-2	Sequence 2, Appl1
39	288.5	26.1	263	1	US-07-906-983-2	Sequence No. 5514787
40	270.5	24.5	128	5	5514582-42	Sequence No. 5514582
41	243.5	22.1	126	5	5514582-43	Sequence No. 5514582
42	229	20.7	62	1	US-08-210-266A-13	Sequence 13, Appl1
43	229	20.7	62	1	US-08-688-675-13	Sequence 13, Appl1
44	229	20.7	62	3	US-08-477-860C-13	Sequence 13, Appl1
45	197	17.8	290	3	US-08-824-692-29	Sequence 29, Appl1

## ALIGNMENTS

RESULT 1  
US-08-356-361-27  
Sequence 27, Application US/08356361  
Patent No. 5833989  
GENERAL INFORMATION:  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman Mary A.  
APPLICANT: Mossakowska, Danuta E.I.  
TITLE OF INVENTION: No. 5833989e1 Compounds  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESS: Smithline Beecham-Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,361  
FILING DATE: 03-Jul-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jervys, Herbert H.  
REGISTRATION NUMBER: 31,171  
REFERENCE/DOCKET NUMBER: P30423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5019  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-356-361-27

Query Match 94.8% Score 1047; DB 2; Length 197;  
Best Local Similarity 94.98; Pred. No. 1.2e-103;  
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
Oy 1 MOCNAPWLPFARPNLTDEFEFFIGTYLNTCEGRGYSRPSITCLKNSVTGAKDRCR 60  
Db 1 MOCNAPWLPFARPNLTDEFEFFIGTYLNTCEGRGYSRPSITCLKNSVTGAKDRCR 60

[illegible]

```

1      RESULT 2
2      US-08-769-967A-27
3      Sequence 27, Application US/08769967A
4      Patent No. 5859223
5      GENERAL INFORMATION:
6      APPLICANT: Mossakowska, Danuta E.I.
7      APPLICANT: Smith, Richard A.G.
8      APPLICANT: Dodd, Ian
9      APPLICANT: Freeman, Anne Mary
10     TITLE OF INVENTION: Soluble CRI Derivatives
11     NUMBER OF SEQUENCES: 33
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: SmithKline Beecham Corporate Intellectual Property
14     STREET: P.O. Box 1539
15     CITY: King of Prussia
16     STATE: Pennsylvania
17     COUNTRY: USA
18     ZIP: 19406
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.25
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/769,967A
26     FILING DATE:
27     CLASSIFICATION: 536
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 08/440,569
30     FILING DATE: 15-May-1995
31     ATTORNEY/AGENT INFORMATION:
32     NAME: King, William T.
33     REGISTRATION NUMBER: 30,954
34     REFERENCE/DOCKET NUMBER: P30423C2
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (610) 270-5364
37     TELEFAX: (610) 270-5090
38     INFORMATION FOR SEQ ID NO: 27:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 197 amino acids
41     TYPE: amino acid
42     TOPOLOGY: linear
43     MOLECULE TYPE: peptide
44     FRAGMENT TYPE: N-terminal
45     US-08-769-967A-27

```

Query Match	94.88;	Score 1047;	DB 2;	Length 197;
Best Local Similarity	94.98;	Pred. No. 1,2e-103;		
Matches 187;	Conservative	2;	Mismatches 8;	Indels 0;
				Gaps 0;
QY	1	MCCNAPEWLPFARPTNLTDGEFFPIGTLYNTECRPEYSGRPSIITLTKNSVTGAKDRCR	60	
DB	1	MCCNAPEWLPFARPTNLTDGEFFPIGTLYNTECRPEYSGRPSIITLTKNSVTGAKDRCR	60	
QY	61	RKSCRNPDPVNGMVAVIRIGIOGSGIRKSCRTGYRLTISSSATCIISDPTVWMDNEPPI	120	
DB	61	RKSCRNPDPVNGMVAVIRIGIOGSGIRKSCRTGYRLTISSSATCIISDPTVWMDNEPPI	120	

OY	121	CDRIPCGLPPIIANGDSTISREFFHGVSVLYTHCNLSGSKKVFELVGPSPSYICNSKD	180
Dd	121	CDRIPCGLPPIITNGDDISTNRKNHFHGSVVTYTRCNGSSGRKFVELVGSPSYICNSND	180
OY	181	QVGIMSGAPPOCIILPNK	197
Dd	181	QVGIMSGAPPOCIILPNK	197

```

1      RESULT      3
2      US-08-356-361-29
3      Sequence 29, Application US/083556361
4      Patent No. 5833989
5      GENERAL INFORMATION:
6      APPLICANT: Smith, Richard A.G.
7      APPLICANT: Dodd, Ian
8      APPLICANT: Freeman Mary A.
9      APPLICANT: Mosakowska, Danuta E.I.
10     TITLE OF INVENTION: No. 5833989el Compounds
11     NUMBER OF SEQUENCES: 31
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Smltkline Beecham-Corporate Intellectual Property
14     STREET: P.O. Box 1539
15     CITY: King of Prussia
16     STATE: Pennsylvania
17     COUNTRY: USA
18     ZIP: 19406
19
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patentin Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/356,361
27     FILING DATE: 03-Jul-1995
28     CLASSIFICATION: 433
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Jervis, Herbert H.
31     REGISTRATION NUMBER: 31,171
32     REFERENCE/DOCKET NUMBER: P30423
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: (610) 270-5019
35     TELEFAX: (610) 270-5050
36     INFORMATION FOR SEQ ID NO: 29:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 254 amino acids
39     TYPE: amino acid
40     TOPOLOGY: linear
41     MOLECULE TYPE: peptide
42     FRAGMENT TYPE: N-terminal
43     US-08-356-361-29

```

	Query Match	Similarity	94.9%	Score 1047	DB 2:	Length 254:
	Best Local	Similarity	94.9%	Pred. No. 1,76-103:		
	Matches 187:	Conservative	2:	Mismatches 8:	Indels 0:	Gaps 0:
QY	1	MCCNAPEWLPFARPNLADFEFFPIGTYLNEYCRPGYSGRPFSITCLNKSWSVTGAKDCR	60			
Db	1	MCCNAPPEWLPFARPNLADFEFFPIGTYLNEYCRPGYSGRPFSITCLNKSWSVTGAKDCR	60			
QY	61	RKSCANPPDPVNGAMVHKIGIOFSQIYSCCKGYRLIGSSATCIIIGDPYIMNENPI	120			
Db	61	RKSCANPPDPVNGAMVHKIGIOFSQIYSCCKGYRLIGSSATCIIIGDPYIMNENPI	120			
QY	121	CRRICGILPPIIANDDEFTSISREYHSGSVVYHONLGSRGKVELYGEPSIYCTSKDD	180			
Db	121	CRRICGILPPIIANDDEFTSISREYHSGSVVYHONLGSRGKVELYGEPSIYCTSKDD	180			
QY	181	QVGIWSGPAPOCIIIPNK	197			
Db	181	QVGIWSGPAPOCIIIPNK	197			



## RESULT 4

US-08-356-361-30  
Sequence 30, Application US/08356361  
Patent No. 5833989  
GENERAL INFORMATION:  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman Mary A.  
APPLICANT: Mossakowska, Danuta E.I.  
TITLE OF INVENTION: No. 5833989el Compounds  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham-Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,361  
FILING DATE: 03-Jul-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jervls, Herbert H.  
REGISTRATION NUMBER: 31,171  
REFERENCE/DOCKET NUMBER: P30423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5019  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ. ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-356-361-30

Query Match 94.8%; Score 1047; DB 2; Length 254;  
Best Local Similarity 94.9%; Pred. No. 1.7e-103;  
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MOCNAPFMLEFARPTNLTDEFFPIGYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60  
DB 1 MOCNAPFMLEFARPTNLTDEFFPIGYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60  
QY 61 RKSCRNPDPVNGVNHVYIKIGIOGSOIKYSGTGYRLIGSSSATCISGDTVIMDNETPI 120  
DB 61 RKSCRNPDPVNGVNHVYIKIGIOGSOIKYSGTGYRLIGSSSATCISGDTVIMDNETPI 120  
QY 121 CDRIPGCLPPTIANGDFTSISREYFHYSVYTYHCNLSGSKKVFELVGEPSIYCTSKDD 180  
DB 121 CDRIPGCLPPTIANGDFTSISREYFHYSVYTYHCNLSGSKKVFELVGEPSIYCTSKDD 180  
QY 181 QVGIMSGPAPQCIIPNK 197  
DB 181 QVGIMSGPAPQCIIPNK 197

## RESULT 5

US-08-769-967A-29  
Sequence 29, Application US/08769967A  
Patent No. 5859223  
GENERAL INFORMATION:  
APPLICANT: Mossakowska, Danuta E.I.  
APPLICANT: Smith, Richard A.G.

APPLICANT: Dodd, Ian  
APPLICANT: Freeman, Anne Mary  
TITLE OF INVENTION: Soluble CRI Derivatives  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,967A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/440,569  
FILING DATE: 15-May-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: KING, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P30423C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5364  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ. ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-769-967A-29

Query Match 94.8%; Score 1047; DB 2; Length 254;  
Best Local Similarity 94.9%; Pred. No. 1.7e-103;  
Matches 187; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MOCNAPFMLEFARPTNLTDEFFPIGYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60  
DB 1 MOCNAPFMLEFARPTNLTDEFFPIGYLYNECRPGYSGRPFSLICLKNVMTGAKDRCR 60  
QY 61 RKSCRNPDPVNGVNHVYIKIGIOGSOIKYSGTGYRLIGSSSATCISGDTVIMDNETPI 120  
DB 61 RKSCRNPDPVNGVNHVYIKIGIOGSOIKYSGTGYRLIGSSSATCISGDTVIMDNETPI 120  
QY 121 CDRIPGCLPPTIANGDFTSISREYFHYSVYTYHCNLSGSKKVFELVGEPSIYCTSKDD 180  
DB 121 CDRIPGCLPPTIANGDFTSISREYFHYSVYTYHCNLSGSKKVFELVGEPSIYCTSKDD 180  
QY 181 QVGIMSGPAPQCIIPNK 197  
DB 181 QVGIMSGPAPQCIIPNK 197

## RESULT 6

US-08-769-967A-30  
Sequence 30, Application US/08769967A  
Patent No. 5859223  
GENERAL INFORMATION:  
APPLICANT: Mossakowska, Danuta E.I.  
APPLICANT: Smith, Richard A.G.  
APPLICANT: Dodd, Ian  
APPLICANT: Freeman, Anne Mary  
TITLE OF INVENTION: Soluble CRI Derivatives  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
STREET: P.O. Box 1539  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,967A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/440,569  
FILING DATE: 15-May-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P30423C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5364  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-769-967A-30

Query Match 94.8%; Score 1047; DB 2; Length 254;  
Best Local Similarity 94.9%; Pred. No. 1.7e-103;  
Matches 187; Conservative 2; Mismatches 83; Indels 0; Gaps 0;

QY 1 MOCNAPEWLPFARPTNLDEFEPIGTLYNECRPGYSGRPSIILKNSVWTGAKRRCR 60  
DB 1 MOCNAPEWLPFARPTNLDEFEPIGTLYNECRPGYSGRPSIILKNSVWTGAKRRCR 60  
QY 61 KSCRNPPDPVNGMVHVYKIQFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPIC 120  
DB 61 KSCRNPPDPVNGMVHVYKIQFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPIC 120  
QY 121 CRIPGCLPPTIANGDFTSISREYFHGVSVYTHCNLGSRGKRVFELVGEPSIYCTSKDD 180  
DB 121 CRIPGCLPPTIANGDFTSISREYFHGVSVYTHCNLGSRGKRVFELVGEPSIYCTSKDD 180  
QY 181 QVGWGPAPQCIIPNK 197  
DB 181 QVGWGPAPQCIIPNK 197

RESULT 7  
5256642-10  
Patent No. 5256642  
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.  
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF  
USE THEREOF  
NUMBER OF SEQUENCES: 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/588,128  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 412,745  
FILING DATE: 26-SEP-1989  
APPLICATION NUMBER: 332,865

FILING DATE: 03-APR-1989  
APPLICATION NUMBER: 176,532  
FILING DATE: 01-APR-1988  
SEQ ID NO: 10;  
LENGTH: 1847  
5256642-10

Query Match 94.4%; Score 1042; DB 5; Length 1847;  
Best Local Similarity 94.9%; Pred. No. 8.6e-102;  
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLDEFEPIGTLYNECRPGYSGRPSIILKNSVWTGAKRRCR 61  
DB 47 QCNAPWLPFARPTNLDEFEPIGTLYNECRPGYSGRPSIILKNSVWTGAKRRCR 106  
QY 62 KSCRNPPDPVNGMVHVYKIQFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPIC 121  
DB 107 KSCRNPPDPVNGMVHVYKIQFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPIC 166  
QY 122 DRIPGCLPPTIANGDFTSISREYFHGVSVYTHCNLGSRGKRVFELVGEPSIYCTSKDD 181  
DB 167 DRIPGCLPPTIANGDFTSISREYFHGVSVYTHCNLGSRGKRVFELVGEPSIYCTSKDD 226  
QY 182 VGIWGPAPQCIIPNK 197  
DB 227 VGIWGPAPQCIIPNK 242

RESULT 8  
5472939-10  
Patent No. 5472939  
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.  
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT  
MEDIATED DISORDERS  
NUMBER OF SEQUENCES: 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/138,825  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 588,128  
FILING DATE: 24-SEP-1990  
APPLICATION NUMBER: 412,745  
FILING DATE: 26-SEP-1989  
APPLICATION NUMBER: 332,865  
FILING DATE: 03-APR-1989  
APPLICATION NUMBER: 176,532  
FILING DATE: 01-APR-1986  
SEQ ID NO: 10;  
LENGTH: 2006  
5472939-10

Query Match 94.4%; Score 1042; DB 5; Length 1847;  
Best Local Similarity 94.9%; Pred. No. 8.6e-102;  
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLDEFEPIGTLYNECRPGYSGRPSIILKNSVWTGAKRRCR 61  
DB 47 QCNAPWLPFARPTNLDEFEPIGTLYNECRPGYSGRPSIILKNSVWTGAKRRCR 106  
QY 62 KSCRNPPDPVNGMVHVYKIQFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPIC 121  
DB 107 KSCRNPPDPVNGMVHVYKIQFGSQIKYSGTKGYRLIGSSSATCIIISGDTYIMDNEPIC 166  
QY 122 DRIPGCLPPTIANGDFTSISREYFHGVSVYTHCNLGSRGKRVFELVGEPSIYCTSKDD 181  
DB 167 DRIPGCLPPTIANGDFTSISREYFHGVSVYTHCNLGSRGKRVFELVGEPSIYCTSKDD 226  
QY 182 VGIWGPAPQCIIPNK 197  
DB 227 VGIWGPAPQCIIPNK 242

Db 227 VGIMSGPAPCIIIPNK 242

RESULT 9

5256642-2

; Patent No. 5256642

; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.

; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
; RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF  
; USE THEREOF

; NUMBER OF SEQUENCES: 30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/588,128

; FILING DATE: 24-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 412,745

; FILING DATE: 26-SEP-1989

; APPLICATION NUMBER: 332,865

; FILING DATE: 03-APR-1989

; APPLICATION NUMBER: 176,532

; FILING DATE: 01-APR-1988

; SEQ ID NO: 2:

LENGTH: 2039

5256642-2

Query Match

Best Local Similarity 94.4%; Score 1042; DB 5; Length 2039;

Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPENLPFARPTNLTDEEFPIGTYLNECRPGYSGRPFSTICLNKNSWTGAKDRCR 61

DB 42 QCNAPENLPFARPTNLTDEEFPIGTYLNECRPGYSGRPFSTICLNKNSWTGAKDRCR 101

QY 62 KSCRNPDPVNGMVAHYKGFQSGQIKYCTGKGRLLGSSSACIIISGDIYIMDNETPIC 121

DB 102 KSCRNPDPVNGMVAHYKGFQSGQIKYCTGKGRLLGSSSACIIISGDIYIMDNETPIC 161

QY 122 DRIPCGLPPTIANGDFTSISREYFHGYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 181

DB 162 DRIPCGLPPTIANGDFTSISREYFHGYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 221

QY 182 VGIMSGPAPCIIIPNK 197

DB 222 VGIMSGPAPCIIIPNK 237

RESULT 10

5472939-2

; Patent No. 5472939

; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.

; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT  
; MEDICATED DISORDERS

; NUMBER OF SEQUENCES: 30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/138,825

; FILING DATE: 19-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 588,128

; FILING DATE: 24-SEP-1990

; APPLICATION NUMBER: 412,745

; FILING DATE: 26-SEP-1989

; APPLICATION NUMBER: 332,865

; FILING DATE: 03-APR-1989

; APPLICATION NUMBER: 176,532

; FILING DATE: 01-APR-1988

; SEQ ID NO: 2:

LENGTH: 2039

5472939-2

Query Match 94.4%; Score 1042; DB 5; Length 2039;  
Best Local Similarity 94.9%; Pred. No. 9,8e-102;  
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPENLPFARPTNLTDEEFPIGTYLNECRPGYSGRPFSTICLNKNSWTGAKDRCR 61

DB 42 QCNAPENLPFARPTNLTDEEFPIGTYLNECRPGYSGRPFSTICLNKNSWTGAKDRCR 101

QY 62 KSCRNPDPVNGMVAHYKGFQSGQIKYCTGKGRLLGSSSACIIISGDIYIMDNETPIC 121

DB 102 KSCRNPDPVNGMVAHYKGFQSGQIKYCTGKGRLLGSSSACIIISGDIYIMDNETPIC 161

QY 122 DRIPCGLPPTIANGDFTSISREYFHGYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 181

DB 162 DRIPCGLPPTIANGDFTSISREYFHGYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 221

QY 182 VGIMSGPAPCIIIPNK 197

DB 222 VGIMSGPAPCIIIPNK 237

RESULT 11

5256642-6

; Patent No. 5256642

; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.

; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
; RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF  
; USE THEREOF

; NUMBER OF SEQUENCES: 30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/588,128

; FILING DATE: 24-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 412,745

; FILING DATE: 26-SEP-1989

; APPLICATION NUMBER: 332,865

; FILING DATE: 03-APR-1989

; APPLICATION NUMBER: 176,532

; FILING DATE: 01-APR-1988

; SEQ ID NO: 6:

LENGTH: 1466

5256642-6

Query Match

Best Local Similarity 71.4%; Score 788; DB 5; Length 1466;

Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps 0;

QY 3 CNAPENLPFARPTNLTDEEFPIGTYLNECRPGYSGRPFSTICLNKNSWTGAKDRCR 62

DB 441 QCNAPENLPFARPTNLTQNASPFPIGTSIKYCRREYIGRPSITCLDLVWSSPDDVCKRK 500

QY 63 SCRNPDPVNGMVAHYKGFQSGQIKYCTGKGRLLGSSSACIIISGDIYIMDNETPIC 122

DB 501 SCRNPDPVNGMVAHYKGFQSGQIKYCTGKGRLLGSSSACIIISGDIYIMDNETPIC 161

QY 123 DRIPCGLPPTIANGDFTSISREYFHGYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 182

DB 561 DRIPCGLPPTIANGDFTSISREYFHGYSVVTYHGNLGRGKRVFELVGEPSIYCTSKDDQ 221

QY 183 VGIMSGPAPCIIIPNK 197

DB 621 VGIMSGPAPCIIIPNK 635

RESULT 12

5472939-6

; Patent No. 5472939

; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.

```

MINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN
H.;MARLIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138, 825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588, 128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412, 745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332, 865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176, 532
FILING DATE: 01-APR-1988
SEQ ID NO: 6:
LENGTH: 1466
5472939-6
Query Match 71.4%; Score 788; DB 5; Length 1466;
Best Local Similarity 72.8%; Pred. No. 5.8e-75;
Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps
0;
QY 3 CNAPEMLFARPTNLTDEFEPIGTLYNTECRPGYSGRPFSTICLKNVWTGAKDRCK 62
Db 441 CQAPHEFFAKLKTQTNASDFIGTSLKYECPREYXGRFSTICLNLVWSSPKDYCKR 500
QY 63 SCRNPPDVVNGVHVHIKIQFGSOIKYCTGKGYRLIGSSAATCIISGDIWINDNETPICD 122
Db 501 SCKTPDPDVGAVHVTIDQVGSRLNYSCTGTRLIGSSAACILSGNTAHSTAPPIQ 560
QY 123 RIPCGLPTIANGDTSISREYFHGVSVYTHCNLGSRCRKVFELVGPSTIYCTSKDOY 182
Db 561 RIPCGLPTIANGDTSISREYFHGVSVYTHCNLGSRCRKVFELVGPSTIYCTSKDOY 620
QY 183 GIVSGAPQCIIPNK 197
Db 621 GIVSGAPQCIIPNK 635
RESULT 13
5256642-5
PATENT NO. 5256642
APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG,
WINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN
H.;MARLIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588, 128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412, 745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332, 865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176, 532
FILING DATE: 01-APR-1988
SEQ ID NO: 5:
LENGTH: 1537
5256642-5
Query Match 71.4%; Score 788; DB 5; Length 1537;
Best Local Similarity 72.8%; Pred. No. 6.1e-75;
Matches 142; Conservative 14; Mismatches 39; Indels 0; Gaps
0;
QY 3 CNAPEMLFARPTNLTDEFEPIGTLYNTECRPGYSGRPFSTICLKNVWTGAKDRCK 62

```

[illegible]



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: January 13, 2001, 13:10:30 ; Search time 72.05 Seconds  
(without alignments)  
185.655 Million cell updates/sec

Title: US-09-380-682-1  
Perfect score: 1104

Sequence: 1 MQCNAPWLPFARPTNLDE.....KDDVGIMSGPAPCIIINRK 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR66:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	94.4	2489	2	I73012 complement C3b/C4b
2	1038	94.0	482	2	A34924 complement C3b/C4b
3	1029	93.2	2014	2	I36936 complement recepto
4	702	63.6	440	2	A43519 complement recepto
5	699	63.3	433	2	A30550 complement C3b/C4b
6	689	62.4	497	2	UC2054 complement regulat
7	674	56.5	676	2	A45900 complement C3b rec
8	474	42.9	381	1	B25975 X/Y protein - mous
9	408	37.0	440	2	B26359 decay-accelerating
10	404	36.6	340	2	I56234 decay-accelerating
11	370.5	33.6	558	2	S57953 decay-accelerating
12	366	33.2	211	2	A46458 human CRI homolog
13	364.5	32.6	610	1	I46001 C4b-binding protei
14	359.5	32.6	597	1	S53711 C4BP alpha chain p
15	342.5	31.0	579	2	A56740 sperm-egg recognit
16	335.5	30.4	1025	1	A43526 complement C3d/Eps
17	325.5	29.5	469	1	NBMS4 C4b-binding protei
18	315.5	28.6	597	1	NBHUC4 C4b-binding protei
19	295	26.7	349	2	G02913 sperm CD46 - human
20	295	26.7	369	2	I57998 membrane cofactor
21	295	26.7	377	2	I54479 membrane cofactor
22	295	26.7	384	2	S01896 membrane cofactor
23	295	26.4	302	1	WMBE1 secretory compleme
24	292	26.4	360	1	WMBE2 membrane-bound com
25	290	26.3	156	2	B30550 complement C3b/C4b
26	288.5	26.1	263	1	MMVZSP complement control
27	286.5	26.0	362	2	JC5194 apolipoprotein H h
28					membrane cofactor

30	286.5	26.0	369	2	JC5138 membrane cofactor
31	284.5	25.8	263	1	C36838 complement control
32	282.5	25.6	263	2	B72152 B18t protein - var
33	282.5	25.6	263	2	T28450 hypothetical prote
34	281	25.5	1091	1	PI0009 complement C3d/Eps
35	251	22.7	1234	1	NBMSH complement factor
36	234.5	21.2	449	1	NBHUS complement factor
37	229	20.7	1231	1	NBHUR complement factor
38	222.5	20.2	560	2	T16833 hypothetical prote
39	222.5	20.2	363	2	B45900 complement C3d/Eps
40	222.5	20.2	1053	2	S46199 probable complemen
41	212	19.2	768	2	A42755 P-selectin precurs
42	212	19.2	768	2	I53821 P-selectin - rat
43	211.5	19.2	868	2	T20239 P-selectin prote
44	188.5	17.1	830	2	A30359 P-selectin - pig
45	187.5	17.0	482	2	JC5092

## ALIGNMENTS

RESULT 1  
I73012  
complement C3b/C4b receptor, membrane-bound form precursor - human  
N:Alternate names: Complement C3b/C4b receptor; complement receptor type 1 (CRI); sur  
N:Contains: Complement C3b/C4b receptor, secreted form  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence revision 24-Nov-1999 #text change 21-Jul-2000  
C:Accession: I73012; I56203; A47602; S03291; S03843; A28507; A24748; C24748  
R:Yik, D.P.; Wong, W.W.  
J. Immunol. 151, 6214-6224, 1993  
A:Title: Structure of the gene for the F allele of complement receptor type 1 and seq  
A:Reference number: I56203; MUID:94065175  
A:Accession: I73012  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-683, 'X', 685-894, 'A', 896-1000, 1451-1471, 'X', 1473-2489 <VIK1>  
A:Cross-references: GB:LI7418; NID:9306678; PIDN:AAB60695.1; PID:9451303  
A:Accession: I56203  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-41 <MON>  
A:Cross-references: GB:X14893  
R:Hourcade, D.; Miesner, D.R.; Atkinson, J.P.; Holes, V.M.  
J. Exp. Med. 168, 1255-1270, 1988  
A:Title: Identification of an alternative polyadenylation site in the human C3b/C4b r  
type 1.  
A:Reference number: S03291; MUID:89010527  
A:Accession: S03291  
A:Molecule type: mRNA  
A:Residues: 26-584 <HOU>  
A:Cross-references: EMBL:X14362; NID:930197; PIDN:CAA32541.1; PID:g736240  
A:Experimental source: Clone CRI-4  
R:Klickstein, L.B.; Bartow, T.J.; Mletic, V.; Rabson, L.D.; Smith, J.A.; Fearon, D.T  
J. Exp. Med. 168, 1699-1717, 1988  
A:Title: Identification of distinct C3b and C4b recognition sites in the human C3b/C4  
A:Reference number: S03843; MUID:89035592  
A:Accession: S03843  
A:Status: translation not shown  
A:Molecule type: RNA  
A:Residues: 1-894, 'A', 896-1000, 1451-2064, 'I', 2066-2276, 'P', 2278-2299, 'H', 2301-2325, 'T  
R:Klickstein, L.B.; Wong, W.W.; Smith, J.A.; Weis, J.H.; Wilson, J.G.; Fearon, D.T.  
J. Exp. Med. 165, 1095-1112, 1987  
A:Title: Human C3b/C4b receptor (CRI). Demonstration of long homologous repeating dom

A:Reference number: A28507; MUID:87168191  
A:Accession: A28507  
A:Molecule type: mRNA  
A:Residues: 933-1221, 'FV',1224-2064, 'I',2066-2276, 'P',2278-2299, 'H',2301-2325, 'T',2327-2347, 'G',2349-2364, 'A',2366-2381, 'C',2383-2398, 'G',2400-2415, 'G',2417-2432, 'A',2434-2449, 'G',2451-2466, 'C',2468-2483, 'G',2485-2500, 'A',2502-2517, 'G',2519-2534, 'A',2536-2551, 'G',2553-2568, 'A',2570-2585, 'G',2587-2602, 'A',2604-2619, 'G',2621-2636, 'A',2638-2653, 'G',2655-2670, 'A',2672-2687, 'G',2689-2704, 'A',2706-2721, 'G',2723-2738, 'A',2740-2755, 'G',2757-2772, 'A',2774-2789, 'G',2791-2806, 'A',2808-2823, 'G',2825-2840, 'A',2842-2857, 'G',2859-2874, 'A',2876-2891, 'G',2893-2908, 'A',2910-2925, 'G',2927-2942, 'A',2944-2959, 'G',2961-2976, 'A',2978-2993, 'G',2995-3010, 'A',3012-3027, 'G',3029-3044, 'A',3046-3061, 'G',3063-3078, 'A',3080-3095, 'G',3097-3112, 'A',3114-3129, 'G',3131-3146, 'A',3148-3163, 'G',3165-3180, 'A',3182-3197, 'G',3200-3215, 'A',3217-3232, 'G',3234-3249, 'A',3251-3266, 'G',3268-3283, 'A',3285-3300, 'G',3302-3317, 'A',3319-3334, 'G',3336-3351, 'A',3353-3368, 'G',3370-3385, 'A',3387-3402, 'G',3404-3419, 'A',3421-3436, 'G',3438-3453, 'A',3455-3470, 'G',3472-3487, 'A',3489-3504, 'G',3506-3521, 'A',3523-3538, 'G',3540-3555, 'A',3557-3572, 'G',3574-3589, 'A',3591-3606, 'G',3608-3623, 'A',3625-3640, 'G',3642-3657, 'A',3659-3674, 'G',3676-3691, 'A',3693-3708, 'G',3710-3725, 'A',3727-3742, 'G',3744-3759, 'A',3761-3776, 'G',3778-3793, 'A',3795-3810, 'G',3812-3827, 'A',3829-3844, 'G',3846-3861, 'A',3863-3878, 'A',3880-3895, 'G',3897-3912, 'A',3914-3929, 'G',3931-3946, 'A',3948-3963, 'G',3965-3980, 'A',3982-3997, 'G',3999-4014, 'A',4016-4031, 'G',4033-4048, 'A',4050-4065, 'G',4067-4082, 'A',4084-4099, 'G',4101-4116, 'A',4118-4133, 'G',4135-4150, 'A',4152-4167, 'G',4169-4184, 'A',4186-4201, 'G',4203-4218, 'A',4220-4235, 'G',4237-4252, 'A',4254-4269, 'G',4271-4286, 'A',4288-4303, 'G',4305-4320, 'A',4322-4337, 'G',4339-4354, 'A',4356-4371, 'G',4373-4388, 'A',4390-4405, 'G',4407-4422, 'A',4424-4439, 'G',4441-4456, 'A',4458-4473, 'G',4475-4490, 'A',4492-4507, 'G',4509-4524, 'A',4526-4541, 'G',4543-4558, 'A',4560-4575, 'G',4577-4592, 'A',4594-4609, 'G',4611-4626, 'A',4628-4643, 'G',4645-4660, 'A',4662-4677, 'G',4679-4694, 'A',4696-4711, 'G',4713-4728, 'A',4730-4745, 'G',4747-4762, 'A',4764-4779, 'G',4781-4796, 'A',4798-4813, 'G',4815-4830, 'A',4832-4847, 'G',4849-4864, 'A',4866-4881, 'G',4883-4898, 'A',4900-4915, 'G',4917-4932, 'A',4934-4949, 'G',4951-4966, 'A',4968-4983, 'G',4985-5000, 'A',5002-5017, 'G',5019-5034, 'A',5036-5051, 'G',5053-5068, 'A',5070-5085, 'G',5087-5102, 'A',5104-5119, 'G',5121-5136, 'A',5138-5153, 'G',5155-5170, 'G',5172-5187, 'A',5189-5204, 'G',5206-5221, 'A',5223-5238, 'G',5240-5255, 'A',5257-5272, 'G',5274-5289, 'A',5291-5306, 'G',5308-5323, 'A',5325-5340, 'G',5342-5357, 'A',5359-5374, 'G',5376-5391, 'A',5393-5408, 'G',5410-5425, 'A',5427-5442, 'G',5444-5459, 'A',5461-5476, 'G',5478-5493, 'A',5495-5510, 'G',5512-5527, 'A',5529-5544, 'G',5546-5561, 'A',5563-5578, 'G',5580-5595, 'A',5597-5612, 'G',5614-5629, 'A',5631-5646, 'G',5648-5663, 'A',5665-5680, 'G',5682-5697, 'A',5699-5714, 'G',5716-5731, 'A',5733-5748, 'G',5750-5765, 'A',5767-5782, 'G',5784-5799, 'A',5801-5816, 'G',5818-5833, 'A',5835-5850, 'G',5852-5867, 'A',5869-5884, 'G',5886-5901, 'A',5903-5918, 'G',5920-5935, 'A',5937-5952, 'G',5954-5969, 'A',5971-5986, 'G',5988-6003, 'A',6005-6020, 'G',6022-6037, 'A',6039-6054, 'G',6056-6071, 'A',6073-6088, 'G',6090-6105, 'A',6107-6122, 'G',6124-6139, 'A',6141-6156, 'G',6158-6173, 'A',6175-6190, 'G',6192-6207, 'A',6209-6224, 'G',6226-6241, 'G',6243-6258, 'A',6260-6275, 'G',6277-6292, 'A',6294-6309, 'G',6311-6326, 'A',6328-6343, 'G',6345-6360, 'A',6362-6377, 'G',6379-6394, 'A',6396-6411, 'G',6413-6428, 'A',6430-6445, 'G',6447-6462, 'A',6464-6479, 'G',6481-6496, 'A',6498-6513, 'G',6515-6530, 'A',6532-6547, 'G',6549-6564, 'A',6566-6581, 'G',6583-6598, 'A',6600-6615, 'G',6617-6632, 'A',6634-6649, 'G',6651-6666, 'A',6668-6683, 'G',6685-6700, 'A',6702-6717, 'G',6719-6734, 'A',6736-6751, 'G',6753-6768, 'A',6770-6785, 'G',6787-6802, 'A',6804-6819, 'G',6821-6836, 'A',6838-6853, 'G',6855-6870, 'A',6872-6887, 'G',6889-6904, 'A',6906-6921, 'G',6923-6938, 'A',6940-6955, 'G',6957-6972, 'A',6974-6989, 'G',6991-7006, 'A',7008-7023, 'G',7025-7040, 'A',7042-7057, 'G',7059-7074, 'A',7076-7091, 'G',7093-7108, 'A',7110-7125, 'G',7127-7142, 'A',7144-7159, 'G',7161-7176, 'A',7178-7193, 'G',7195-7210, 'A',7212-7227, 'G',7229-7244, 'A',7246-7261, 'G',7263-7278, 'A',7280-7295, 'G',7297-7312, 'A',7314-7329, 'G',7331-7346, 'A',7348-7363, 'G',7365-7380, 'A',7382-7397, 'G',7400-7415, 'A',7417-7432, 'G',7434-7449, 'A',7451-7466, 'G',7468-7483, 'A',7485-7500, 'G',7502-7517, 'A',7519-7534, 'G

```

Db      102 KSCRNPDPVNGVAVHVIKIGFQSGQIKYKSCTRGRLIGSSSNTCLISDGYIWMDETIC 161
Oy      122 DRPGCLPPTIANGDPTISREYFHGVSYYVYHCLNGSKKVFELVGPSTYCTSKDDQ 181
Db      162 DRPGCLPPTIANGDPTISREYFHGVSYYVYHCLNGSKKVFELVGPSTYCTSKDDQ 221
Oy      182 VGIWSGPAPQCIIIPNK 197
Db      222 VGIWSGPAPQCIIIPNK 237

RESULT      2
A34924
complement C3b/C4b receptor-like protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jul-1990 #sequence_revision 11-Apr-1997 #text_change 03-Dec-1999
C:Accession: A34924; S03292
R:Hourcade, D.; Miesner, D.R.; Bee, C.; Zeldes, W.; Atkinson, J.P.
J. Biol. Chem. 265, 974-980, 1990
A>Title: Duplication and divergence of the amino-terminal coding region of the complement C3b/C4b receptor-like protein precursor
A:Reference number: A34924; MUID:90110163
A:Accession: A34924
A:Molecule type: DNA
A:Residues: 1-479 <HO>
A:Cross-references: GB:J05195
R:Hourcade, D.; Miesner, D.R.; Atkinson, J.P.; Holers, V.M.
J. Exp. Med. 168, 1255-1270, 1988
A>Title: Identification of an alternative polyadenylation site in the human C3b/C4b receptor-like protein precursor
A:Reference number: S03291; MUID:89010527
A:Accession: S03292
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 77FFFAFR, 452-482 <HO>
A:Cross-references: EMBL:X14360
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1988
F:43-99/Domain: complement factor H repeat homology <FH01>
F:104-161/Domain: complement factor H repeat homology <FH02>
F:166-233/Domain: complement factor H repeat homology <FH03>
F:238-293/Domain: complement factor H repeat homology <FH04>
F:297-353/Domain: complement factor H repeat homology <FH05>
F:358-416/Domain: complement factor H repeat homology <FH06>
F:421-478/Domain: complement factor H repeat homology <FH07>

Query Match      94.0%; Score 1038; DB 2; Length 482;
Best Local Similarity 93.9%; Pred. No. 1.5e-85;
Matches 184; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy      2  OCNAPEMFARPNLTDEEFFPIGTILNLCRGGYSGRPSITCLKNSWGTAKDRCR 61
Db      42  OCNPEWLPFARPNLTDEEFFPIGTILNLCRGGYSGRPSITCLKNSWTSKDKCR 101
Oy      62  KSCRNPDPVNGVAVHVIKIGFQSGQIKYKSCTRGRLIGSSSNTCLISDGYIWMDETIC 121
Db      102 KSCRNPDPVNGVAVHVIKIDIFRSQIKYKSCGRRLIGSSSNTCLISGNTYIMDKTPVC 161
Oy      122 DRPGCLPPTIANGDPTISREYFHGVSYYVYHCLNGSKKVFELVGPSTYCTSKDDQ 181
Db      162 DRPGCLPPTIANGDPTISREYFHGVSYYVYHCLNGSKKVFELVGPSTYCTSKDDQ 221
Oy      182 VGIWSGPAPQCIIIPNK 197
Db      222 VGIWSGPAPQCIIIPNK 237

RESULT      3
I36936
complement receptor 1 - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I36936; I36937

```



R. Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.; Atkinson, J.P.  
J. Immunol. 153, 691-700, 1994  
A.Title: Primary sequence of an alternatively spliced form of CRI. Candidate for the 75,  
A.Reference number: I16935; MUID:94292799  
A.Accession: I16936  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-2014 <BIR1>  
A.Cross-references: GB:I16920; NID:9551564; PIDN:AA51438.1; PID:9557725  
A.Accession: I16937  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-397,1751-2014 <BIR2>  
A.Cross-references: GB:I16921; NID:9557726; PIDN:AA51439.1; PID:9557727  
A.Genetics:  
A.Gene: CRI  
C.Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology  
C.Keywords: duplication; glycoprotein; tandem repeat  
F:18-74/Domain: complement factor H repeat homology <FH01>  
F:79-136/Domain: complement factor H repeat homology <FH02>  
F:141-207/Domain: complement factor H repeat homology <FH03>  
F:213-268/Domain: complement factor H repeat homology <FH04>  
F:272-328/Domain: complement factor H repeat homology <FH05>  
F:333-391/Domain: complement factor H repeat homology <FH06>  
F:396-462/Domain: complement factor H repeat homology <FH07>  
F:470-526/Domain: complement factor H repeat homology <FH08>  
F:529-586/Domain: complement factor H repeat homology <FH09>  
F:722-778/Domain: complement factor H repeat homology <FH10>  
F:1041-1107/Domain: complement factor H repeat homology <FH11>  
F:1172-1228/Domain: complement factor H repeat homology <FH12>  
F:1233-1291/Domain: complement factor H repeat homology <FH13>  
F:1296-1362/Domain: complement factor H repeat homology <FH14>  
F:1432-1489/Domain: complement factor H repeat homology <FH15>  
F:1645-1681/Domain: complement factor H repeat homology <FH16>  
F:1749-1815/Domain: complement factor H repeat homology <FH17>  
F:1833-1879/Domain: complement factor H repeat homology <FH18>  
F:1884-1940/Domain: complement factor H repeat homology <FH19>

Query Match 93.2%; Score 1029; DB 2; Length 2014;  
Best Local Similarity 93.9%; Pred. No. 4,4e-84;  
Matches 184; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 QCNAPFWLPFARPTNLTDEFFPIGTLYNECRPGYSGRPFSTICLKNVWTGAKRCRR 61  
DB 17 QCNAPFWLPFARPTNLTDEFFPIGTLYNECRPGYSGRPFSTICLKNVWTGAKRCRR 76  
QY 62 KCRNPDPVNGVAVHYIKIGFQSGQIKYSGCTKGYRLIGSSSACITISGDTIVMDNETPIC 121  
DB 77 KCRNPDPVNGVAVHYIKIGFQSGQIKYSGCTKGYRLIGSSSACITISGDTIVMDNETPIC 136  
QY 122 DRIPGCLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 181  
DB 137 DRIPGCLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 196  
QY 182 VGWSPAPQCIIPNK 197  
DB 197 VGWSPAPQCIIPNK 212

RESULT 4  
A43519  
complement receptor CRI precursor - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 28-Oct-1992 #sequence\_revision 30-Jan-1993 #text\_change 19-May-2000  
C.Accession: A43519  
J.Paul, M.S.; Aegeerter, M.; Cepek, K.; Miller, M.D.; Wells, J.H.  
J. Immunol. 144, 1988-1996, 1990  
A.Title: The murine complement receptor gene family. The genomic and transcriptional com  
A.Reference number: A43519; MUID:90171600  
A.Status: preliminary  
A.Molecule type: DNA

A.Residues: 1-440 <PAU>  
A.Cross-references: GB:M34164  
A.Note: The authors translated the codon GGC for residue 21 as Ala, and CAG for resid  
C.Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology  
F:42-98/Domain: complement factor H repeat homology <FH1>  
F:103-160/Domain: complement factor H repeat homology <FH2>  
F:165-231/Domain: complement factor H repeat homology <FH3>  
F:237-293/Domain: complement factor H repeat homology <FH4>  
F:299-355/Domain: complement factor H repeat homology <FH5>

Query Match 63.6%; Score 702; DB 2; Length 440;  
Best Local Similarity 63.1%; Pred. No. 1.8e-55;  
Matches 124; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

QY 3 CNAPEWLPFARPTNLTDEFFPIGTLYNECRPGYSGRPFSTICLKNVWTGAKRCRR 62  
DB 42 CPAPQSPAKPNTLDESMFPIGTLYLCELPYIKRPFSTICKQDSTWTSADKCIK 101  
QY 63 SCRNPPDPVNGVAVHYIKIGFQSGQIKYSGCTKGYRLIGSSSACITISGDTIVMDNETPIC 122  
DB 102 QKTPSDPENGLVHVTGIFGSRINVTGCGYRLIGSSSACITISGDTIVMDNETPIC 161  
QY 123 RIPCGLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 182  
DB 162 WIPCEIPGIPNGDFSSSTREDFHGMVYTYRCNTDARKALFNLVGEPSICTSKDDQ 221  
QY 183 GWSGPPQCIIPNK 197  
DB 222 GWSGPPQCIIPNK 236

RESULT 5  
A30550  
complement C3b/C4b receptor precursor - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 03-Mar-1989 #sequence\_revision 03-Mar-1989 #text\_change 19-May-2000  
C.Accession: A30550  
J.Paul, M.S.; Aegeerter, M.; O'Brien, S.E.; Kurtz, C.B.; Wells, J.H.  
J. Immunol. 142, 582-589, 1989  
A.Title: The murine complement receptor gene family. Analysis of mCRY gene products a  
A.Reference number: A30550; MUID:89093944  
A.Accession: A30550  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-433 <PAU>  
C.Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology  
F:42-98/Domain: complement factor H repeat homology <FH1>  
F:103-160/Domain: complement factor H repeat homology <FH2>  
F:165-231/Domain: complement factor H repeat homology <FH3>  
F:237-293/Domain: complement factor H repeat homology <FH4>  
F:299-355/Domain: complement factor H repeat homology <FH5>

Query Match 63.3%; Score 699; DB 2; Length 433;  
Best Local Similarity 63.1%; Pred. No. 3.2e-55;  
Matches 123; Conservative 23; Mismatches 49; Indels 0; Gaps 0;

QY 3 CNAPEWLPFARPTNLTDEFFPIGTLYNECRPGYSGRPFSTICLKNVWTGAKRCRR 62  
DB 42 CPAPQSPAKPNTLDESMFPIGTLYLCELPYIKRPFSTICKQDSTWTSADKCIK 101  
QY 63 SCRNPPDPVNGVAVHYIKIGFQSGQIKYSGCTKGYRLIGSSSACITISGDTIVMDNETPIC 122  
DB 102 QKTPSDPENGLVHVTGIFGSRINVTGCGYRLIGSSSACITISGDTIVMDNETPIC 161  
QY 123 RIPCGLPTIANGDFTSISREYFHGVSYYTYHCNLSGRKKVFLVGEPSICTSKDDQ 182  
DB 162 WIPCEIPGIPNGDFSSSTREDFHGMVYTYRCNTDARKALFNLVGEPSICTSKDDQ 221  
QY 183 GWSGPPQCIIPNK 197  
DB 222 GWSGPPQCIIPNK 236



QY	129	PTTANGDFTSISREYF	145
QY	69	DPVNMVAVHVGIOGSGIKYKSCFGYRLIISSSSATCIISGTGVIMWDEPFIQDIPGCL	128
Db	254	DPENLVAVHVGIEGSGININTCNGYRLIISSSSAVCVITIDOSVDMDEAPICWIPCEI	313
Db	314	PGGINDGFSSSTREDF	330
RESULT	9		
		B26359	
		decay-accelerating factor, GPI-anchored splice form precursor - human	
		N:Alternate names: CD55; DAF splice form 2; decay-accelerating factor membrane-bound form	
		C:Species: Homo sapiens (man)	
		C:Date: 05-Oct-1998 #sequence_revision 16-Aug-1996 #text_change 02-Jun-2000	
		C:Accession: B26359; A27666; A39101; I52594; I52564	
		R:Caras, I.W.; Davitz, M.A.; Rhee, L.; Meddell, G.; Martin Jr., D.W.; Nussenzweig, V.	
		Nature 325, 545-549, 1987	
		A:Title: Cloning of decay-accelerating factor suggests novel use of splicing to generated	
		A:Reference number: A26359; MUID:87115845	
		A:Accession: B26359	
		A:Molecule type: mRNA	
		A:Residues: 1-381 <CAR>	
		A:Cross-references: GB:W0142; NID:g181464; PID:AAA52168.1; PID:g181465	
		R:Medof, M.E.; Lublin, D.M.; Holers, V.M.; Ayers, D.J.; Getty, R.R.; Leykam, J.F.; Atkinson	
		Proc. Natl. Acad. Sci. U.S.A. 84, 2007-2011, 1987	
		A:Title: Cloning and characterization of cDNAs encoding the complete sequence of decay-ac	
		A:Reference number: A27666; MUID:87115602	
		A:Accession: A27666	
		A:Molecule type: mRNA	
		A:Residues: 6-79, 'T', 81-84, 'W', 86-381 <MED>	
		A:Cross-references: GB:M15799; NID:g181462; PID:AAA52167.1; PID:g181463	
		R:Moran, P.; Raab, H.; Kohr, W.J.; Caras, I.W.	
		J. Biol. Chem. 266, 1250-1257, 1991	
		A:Title: Glycophospholipid membrane anchor attachment. Molecular analysis of the cleavag	
		A:Reference number: A39101; MUID:91093238	
		A:Accession: A39101	
		A:Molecule type: protein	
		A:Residues: 338-352 <MOR>	
		R:Lublin, D.M.; Mallinson, G.; Poole, J.; Reid, M.E.; Thompson, E.S.; Ferdman, B.R.; Tel	
		Blood 84, 1276-1282, 1994	
		A:Title: Molecular basis of reduced or absent expression of decay-accelerating factor in	
		A:Reference number: I52564; MUID:94325573	
		A:Accession: I52564	
		A>Status: translated from GB/EMBL/DBJ	
		A:Molecule type: DNA	
		A:Residues: 194-198 'L', 200-209 <LUB>	
		A:Cross-references: GB:S72858; NID:g639599; PID:MAC60633.1; PID:g639600	
		A:Experimental source: Individual KW, Cromer blood group phenotype Dr(a-)	
		A:Note: the single nucleotide difference in this allele, which changes Ser-199 to Leu, 1	
		on (see reference I52564), and thus reduced DAF expression	
		R:Reid, M.E.; Mallinson, G.; SIm, R.B.; Poole, J.; Pausch, V.; Merry, A.H.; Llew, Y.W.;	
		Blood 79, 3291-3297, 1991	
		A:Title: Biochemical studies on red blood cells from a patient with the Imab phenotype (	
		A:Reference number: I52564; MUID:92075980	
		A:Accession: I52564	
		A>Status: translated from GB/EMBL/DBJ	
		A:Molecule type: mRNA	
		A:Residues: 190-193 'OLCPVE', <RE2>	
		A:Cross-references: GB:S70688; NID:g240301; PID:AMB20576.1; PID:g240302	
		A:Experimental source: Individual KW, Cromer blood group phenotype Dr(a-) (described immu	
		C:Comment: Cromer blood group system antigens reside on this protein.	
		C:Comment: For an alternative splice form, see PIR:A26359	
		C:Genetics:	
		A:Gene: GDB:DAF	
		A:Cross-references: GDB:119088; OMTM:125240	
		A:Map position: Iq32-Iq32	
		C:Function:	
		A:Description: protects tissues from damage by regulating complement activation on cell	
		A:Superfamily: decay-accelerating factor; complement factor H repeat homology	
		C:Keywords: alternative splicing; blocked carboxyl end; complement inhibitor; glycoprote	
		I:34/Domain: signal sequence #status predicted <SIG>	
		I:35-35/Product: decay-accelerating factor 2 #status predicted <MAT>	

```

F:36-94/Domain: complement factor H repeat homology <FH01>
F:98-158/Domain: complement factor H repeat homology <FH02>
F:163-220/Domain: complement factor H repeat homology <FH03>
F:225-283/Domain: complement factor H repeat homology <FH04>
F:354-381/Domain: carboxyl-terminal propeptide #status predicted <PRO>
F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:355/Modified site: GPI anchor ethanolamine amidated carboxyl end (Ser) (in mature f
Query Match          37.0%; Score 408; DB 1; Length 381;
Best Local Similarity 42.6%; Pred. No. 3,5e-29;
Matches      83; Conservative    29; Mismatches   69; Indels    14; Gaps     6;

OY      3 CNAPEMLPFA--RPTNLDEFEFFPIGYLTNCEKRGYSGRPF---SIIELKNVWTGAKD 57
           :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
DB      98 CEVPRLNSASIKQIYYITQN-FPVGIWVEYECRGYRRPSLPLKLICLNLMKSTAVE 156
OY      58 RCRKRSCKNPDPVNGMWHVTKIGIOFGSQIKYISCTKGRIILGSSSATCIISGDVIYMDNE 117
           ||::||::||::||::||::||::||::||::||::||::||::||::||:
DB      157 FCKRKSCNPPEIRNGQIDVPGGLIFGATISFCSTGKYLGSTSFLLIGSSSVOWSDP 216
OY      118 TPICRICGEPPTIANGDFTSISEHYHVSVTYHTCNLSRGKVLELVGEPSICTS 177
           ||::||::||::||::||::||::||::||::||::||::||::||::||:
DB      217 LPECEETICPAFPQIDNKIIQG-ERDHIGYQSOTTYACNK-----FTMIGHSHIICTV 269
OY      178 KDDYGIVSGAPQC 192
           ::||::||::||::||::||::||::||::||::||::||::||::||:
DB      270 NNDE-GEMSGPPPEC 283

RESULT 10
A26359
decay-accelerating factor, splice form 1 precursor - human
N:Alternate names: decay-accelerating factor 5; decay-accelerating factor secreted fo
C:Species: Homo sapiens (mac)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Jun-2000
C:Accession: A26359; A39702; S16187; S23138; A27258
R:Caras, I.W.; Davlitz, M.A.; Rhee, L.; Meddell, G.; Martin Jr., D.W.; Nussenzweig, V.
Nature 325, 545-549, 1987
A>Title: Cloning of decay-accelerating factor suggests novel use of splicing to gener
A:Reference number: A26359; MUID:87115845
A:Accession: A26359
A:Molecule type: mRNA
A:Residues: 1-440 <CAR>
A:Cross-references: GB:M30142
R:Emlon U.K.; Ravl, L.; Medof, M.E
Proc. Natl. Acad. Sci. U.S.A. 88, 4675-4679, 1991
A>Title: Characterization of the decay-accelerating factor gene promoter region.
A:Reference number: A39702; MUID:91271256
A:Accession: A39702
A:Molecule type: DNA
A:Residues: 1-79,'T',81-104 <END>
A:Cross-references: GB:M64356
A>Note: The authors translated the codon AGT for residue 85 as Met
R:Nakano, Y.; Sugita, Y.; Ishikawa, Y.; Choi, N.H.; Tobe, T.; Tomita, M.
Biochim. Biophys. Acta 1074, 326-330, 1991
A>Title: Isolation of two forms of decay-accelerating factor (DAF) from human urine.
A:Reference number: S16187; MUID:91291869
A:Accession: S16187
A>Status: preliminary
A:Molecule type: protein
A:Residues: 35-47 <BIO>
R:Nakano, Y.; Sumida, K.; Kikuta, N.; Miura, N.H.; Tobe, T.; Tomita, M.
Biochim. Biophys. Acta 1116, 235-240, 1992
A>Title: Complete determination of disulfide bonds localized within the short consensu
A:Reference number: S23138; MUID:92305034
A:Accession: S23138
A>Status: preliminary
A:Molecule type: protein
A:Residues: 35-41,65-68,79-81,93-103,128-134,143-145,155-159,162-168,188-192,203-204;
R:Sugita, Y.; Negrozi, T.; Matsuda, T.; Sakamoto, T.; Tomita, M.
J. Biochem. 100, 143-150, 1986
A>Title: Improved method for the isolation and preliminary characterization of human

```





**THIS PAGE BLANK (USPTO)**

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2001, 13:41:15 ; Search time 32.86 Seconds  
(without alignments)  
193.607 Million cell updates/sec

Title: US-09-380-682-1

Perfect score: 1104  
Sequence: 1 MGNAPFWLFFARPTNLTDE.....KDOGVGIMSGPAPQCIIIPNK 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1042	94.4	2039 1	CRI_HUMAN
2	437.5	39.6	390 1	DAF1_MOUSE
3	413.5	37.5	407 1	DAF2_MOUSE
4	408	37.0	381 1	DAF_HUMAN
5	404	36.6	340 1	DAF_PONPY
6	370.5	33.6	558 1	C4BP_RAT
7	364.5	33.0	507 1	DAF_CAVPO
8	364.5	33.0	610 1	CR2_BOVIN
9	335.5	30.4	1025 1	CR2_MOUSE
10	325.5	29.5	469 1	C4BP_MOUSE
11	315.5	28.6	597 1	C4BP_HUMAN
12	295	26.7	377 1	MCP_HUMAN
13	292	26.4	360 1	CCPH_HSVSA
14	290.5	26.3	1033 1	CR2_HUMAN
15	288.5	25.1	263 1	VCP_VACCV
16	251	22.7	1234 1	CFRH_MOUSE
17	234.5	21.2	1231 1	CFRH_HUMAN
18	212	19.2	768 1	LEM3_MOUSE
19	212	19.2	768 1	LEM3_RAT
20	200.5	18.2	769 1	LEM3_SHEEP
21	188.5	17.1	830 1	LEM3_HUMAN
22	187.5	17.0	484 1	LEM2_PIG
23	187.5	17.0	668 1	F13B_MOUSE
24	187	16.9	611 1	LEM2_CANFA
25	186	16.8	646 1	LEM3_BOVIN
26	183	16.6	610 1	LEM2_HUMAN
27	182.5	16.5	551 1	LEM2_RABIT
28	176.5	16.0	331 1	CFHD_HUMAN
29	176	15.9	258 1	C4BB_HUMAN
30	176	15.9	958 1	H1G_PROMO
31	173	15.7	1919 1	LFC_CARO
32	172.5	15.6	330 1	CFH1_HUMAN
33	172	15.6	345 1	APOH_CANFA

## ALIGNMENTS

```

RESULT 1
ID CRI_HUMAN
AC P17927:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3b/C4b RECEPTOR) (CD35
DE ANTIGEN).
GN CRI OR C3bR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8903592; PubMed=2972794;
RA Klinkstein L.B., Barlow T.J., Miletic V., Rabson L.D., Smith J.A.,
RA Fearon D.T.;
RT "Identification of distinct C3b and C4b recognition sites in the
RT human C3b/C4b receptor (CRI, CD35) by deletion mutagenesis.";
RL J. Exp. Med. 168:1699-1717(1988).
RN [2]
RP SEQUENCE OF 503-2039 FROM N.A.
RX MEDLINE=87168191; PubMed=2951479;
RA Klinkstein L.B., Wong W.W., Smith J.A., Wels J.H., Wilson J.G.,
RA Fearon D.T.;
RT "Human C3b/C4b receptor (CRI). Demonstration of long homologous
RT repeating domains that are composed of the short consensus repeats
RT characteristics of C3/C4 binding proteins.";
RL J. Exp. Med. 165:1095-1112(1987).
RN [3]
RP SEQUENCE OF 761-783; 831-845 AND 1179-1195 FROM N.A.
RX MEDLINE=86067975; PubMed=2933745;
RA Wong W.W., Klinkstein L.B., Smith J.A., Wels J.H., Fearon D.T.;
RT "Identification of a partial cDNA clone for the human receptor for
RT complement fragments C3b/C4b.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7711-7715(1985).
CC -!- FUNCTION: CRI, PRESENT ON ERYTHROCYTES, LEUCOCYTES, GLOMERULAR
CC PODOCYTES, AND SPLENIC FOLLICULAR DENDRITIC CELLS, MEDIATES THE
CC BINDING BY THESE CELLS OF PARTICLES AND IMMUNE COMPLEXES THAT HAVE
CC ACTIVATED COMPLEMENT.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOX BLOOD GROUP SYSTEM.
CC -!- MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A
CC LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A
CC CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
CC TWO SRCS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
CC SPECIFICITY.
CC -!- MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F ALLOTYPE OF CRI.
CC -!- SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

FT	DISULFID	297	340		BY SIMILARITY.
FT	DISULFID	326	353		BY SIMILARITY.
FT	DISULFID	358	400		BY SIMILARITY.
FT	DISULFID	386	416		BY SIMILARITY.
FT	DISULFID	421	470		BY SIMILARITY.
FT	DISULFID	450	487		BY SIMILARITY.
FT	DISULFID	493	536		BY SIMILARITY.
FT	DISULFID	523	549		BY SIMILARITY.
FT	DISULFID	554	595		BY SIMILARITY.
FT	DISULFID	581	611		BY SIMILARITY.
FT	DISULFID	616	665		BY SIMILARITY.
FT	DISULFID	645	682		BY SIMILARITY.
FT	DISULFID	688	730		BY SIMILARITY.
FT	DISULFID	716	743		BY SIMILARITY.
FT	DISULFID	747	790		BY SIMILARITY.
FT	DISULFID	776	803		BY SIMILARITY.
FT	DISULFID	808	850		BY SIMILARITY.
FT	DISULFID	836	866		BY SIMILARITY.
FT	DISULFID	871	920		BY SIMILARITY.
FT	DISULFID	900	937		BY SIMILARITY.
FT	DISULFID	943	986		BY SIMILARITY.
FT	DISULFID	973	999		BY SIMILARITY.
FT	DISULFID	1004	1045		BY SIMILARITY.
FT	DISULFID	1031	1061		BY SIMILARITY.
FT	DISULFID	1066	1115		BY SIMILARITY.
FT	DISULFID	1095	1132		BY SIMILARITY.
FT	DISULFID	1138	1180		BY SIMILARITY.
FT	DISULFID	1166	1193		BY SIMILARITY.
FT	DISULFID	1197	1240		BY SIMILARITY.
FT	DISULFID	1226	1253		BY SIMILARITY.
FT	DISULFID	1258	1300		BY SIMILARITY.
FT	DISULFID	1286	1316		BY SIMILARITY.
FT	DISULFID	1321	1370		BY SIMILARITY.
FT	DISULFID	1350	1387		BY SIMILARITY.
FT	DISULFID	1396	1439		BY SIMILARITY.
FT	DISULFID	1426	1452		BY SIMILARITY.
FT	DISULFID	1457	1498		BY SIMILARITY.
FT	DISULFID	1484	1514		BY SIMILARITY.
FT	DISULFID	1519	1568		BY SIMILARITY.
FT	DISULFID	1548	1585		BY SIMILARITY.
FT	DISULFID	1591	1633		BY SIMILARITY.
FT	DISULFID	1619	1646		BY SIMILARITY.
FT	DISULFID	1650	1693		BY SIMILARITY.
FT	DISULFID	1679	1706		BY SIMILARITY.
FT	DISULFID	1711	1753		BY SIMILARITY.
FT	DISULFID	1739	1769		BY SIMILARITY.
FT	DISULFID	1774	1823		BY SIMILARITY.
FT	DISULFID	1803	1840		BY SIMILARITY.
FT	DISULFID	1848	1891		BY SIMILARITY.
FT	DISULFID	1877	1904		BY SIMILARITY.
FT	DISULFID	1909	1952		BY SIMILARITY.
FT	DISULFID	1938	1965		BY SIMILARITY.
FT	CARBOHYD	56	56		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	252	252		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	410	410		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	447	447		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	509	509		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	578	578		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	702	702		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	860	860		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	897	897		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	959	959		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1028	1028		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1152	1152		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1310	1310		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1481	1481		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1504	1504		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1534	1534		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1540	1540		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1605	1605		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1763	1763		N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	1908	1908		N-LINKED (GLCNAC. .) (POTENTIAL)
AA:	223589				
SEQUENCE	3039				
MM:	B2FD29B6BD3C5EB7				
CRG64:					



Query Match 94.4%; Score 1042; DB 1; Length 2039;  
 Best Local Similarity 94.9%; Pred. No. 1,1e-87;  
 Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNPPEWLPAPRPTNLDEFEPIGTLYLNECRPGYSGRPSSICLNKSVTGAKDCGR 61  
 |||||  
 DB 42 QCNPPEWLPAPRPTNLDEFEPIGTLYLNECRPGYSGRPSSICLNKSVTGAKDCGR 101  
 |||||

QY 62 KSCNPPDPVNGVHVHVIKIQFGSQIKYSCYRLIGSSATCIISGDTYIMDNPTPIC 121  
 |||||  
 DB 102 KSCNPPDPVNGVHVHVIKIQFGSQIKYSCYRLIGSSATCIISGDTYIMDNPTPIC 161  
 |||||

QY 122 DRIPCGPLPTIANGDFTSISREHYGVSVTYHGNLGRKRVLYGEPSTYCTSDQ 181  
 |||||  
 DB 162 DRIPCGPLPTIANGDFTSISREHYGVSVTYHGNLGRKRVLYGEPSTYCTSDQ 221  
 |||||

QY 182 VGIMSGPAPCIIIPNK 197  
 |||||  
 DB 222 VGIMSGPAPCIIIPNK 237  
 |||||

RESULT 2  
 ID DAF1\_MOUSE STANDARD; PRT; 390 AA.  
 AC 061475; 061397; p97732;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE COMPLEMENT DECAY-ACCELERATING FACTOR, GPI-ANCHORED PRECURSOR  
 DE (DAF-GPI).  
 GN DAF1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE-TESTIS;  
 RA MEDLINE-95403982; PubMed-7545711;  
 RA Spicer A.P., Seidlin M.F., Gendler S.J.;  
 RT "Molecular cloning and chromosomal localization of the mouse decay-  
 RT accelerating factor genes. Duplicated genes encode  
 RT glycosylphosphatidylinositol-anchored and transmembrane forms.";  
 RT J. Immunol. 155:3079-3091(1995).  
 RN [2]  
 RP SEQUENCE OF 7-390 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-SPLEEN;  
 RA MEDLINE-96362213; PubMed-8671624;  
 RA Fukuda Y., Yasui A., Okada N., Okada H.;  
 RT "Molecular cloning of murine decay accelerating factor by  
 RT immunoscreening.";  
 RT Int. Immunol. 8:379-385(1996).  
 CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.  
 CC -1- TISSUE SPECIFICITY: BRAIN, SECRETORY EPITHELIA, SKELETAL MUSCLE,  
 CC LIVER, TESTES, THYMUS, SPLEEN AND LYMPH NODE.  
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR  
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE  
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.  
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION  
 CC (RCA) FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: LA1366; AAB0091.1; -

DR EMBL: D63679; BAA09830.1; -  
 DR .HSSP: P08603; 1HCC.  
 DR WGD; MG1:104850; DAF1.  
 DR INTERPRO: IPR000436; -  
 DR PIRAM: PF00084; sush1; 4.  
 KW Complement pathway; Glycoprotein; Membrane; Repeat; GPI-anchor;  
 KM Signal; Sush1.  
 FT SIGNAL 1 34  
 FT CHAIN 35 361  
 FT  
 FT PROPER 362 390  
 FT DOMAIN 35 285  
 FT REPEAT 35 95  
 FT REPEAT 97 159  
 FT REPEAT 162 221  
 FT REPEAT 224 285  
 FT DOMAIN 288 364  
 FT DISULFID 65 94  
 FT DISULFID 98 145  
 FT DISULFID 129 158  
 FT DISULFID 163 204  
 FT DISULFID 190 220  
 FT DISULFID 225 267  
 FT DISULFID 253 284  
 FT CARBOHYD 187 187  
 FT CARBOHYD 262 262  
 FT LIPID 361 361  
 FT CONFLICT 7 7  
 FT CONFLICT 9 9  
 FT CONFLICT 83 83  
 FT CONFLICT 91 91  
 FT CONFLICT 135 135  
 FT CONFLICT 173 173  
 FT CONFLICT 180 180  
 SQ SEQUENCE 390 AA; 42618 MW; 4418722DFF47F9E7 CRC64;

Query Match 39.6%; Score 437.5; DB 1; Length 390;  
 Best Local Similarity 44.7%; Pred. No. 5.2e-33;  
 Matches 92; Conservative 25; Mismatches 68; Indels 21; Gaps 6;

QY 3 QCNPPEWLPAPRPTNLDEFEPIGTLYLNECRPGYSGR---PSIICLNKSVTG 55  
 |||||  
 DB 98 CVAPERLSFA---SLKEYINMNEFPVGTIVEYECRGRFGEQPLPKATCLELWSPV 154  
 |||||

QY 56 KDCRRKSCNPPDPVNGVHVHVIKIQFGSQIKYSCYRLIGSSATCIISGDTYIMD 115  
 |||||  
 DB 155 AQFRRKSCNPPDPVNGVHVHVIKIQFGSQIKYSCYRLIGSSATCIISGDTYIMD 214  
 |||||

QY 116 NEPTICDRIPCGPLPTIANGDFTSISREHYGVSVTYHGNLGRKRVLYGEPSTYCT 175  
 |||||  
 DB 215 DEFPVCTEICHPEPPTKINNGIMRGSDSY--TYSQVVTYSCDKG-----FLVGNASTYC 267  
 |||||

QY 176 TSKDDVGIWGPAPCIIIPNK 197  
 |||||  
 DB 268 TVSKSDVGIWGPAPCIIIPNK 293  
 |||||

RESULT 3  
 ID DAF2\_MOUSE STANDARD; PRT; 407 AA.  
 AC 061476;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE COMPLEMENT DECAY-ACCELERATING FACTOR, TRANSMEMBRANE PRECURSOR  
 DE (DAF-TM).  
 GN DAF2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.



RA Lublin D.M., Mallinson G., Poole J., Reid M.E., Thompson E.S.,  
 RA Ferdman B.R., Telen M.J., Anstee D.J., Tanner M.J.A.;  
 RT "Molecular basis of reduced or absent expression of  
 RT decay-accelerating factor in Cromer blood group phenotypes.";  
 RL Blood 84:1276-1282(1994).  
 CC -1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT  
 CC CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT  
 CC C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.  
 CC INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES  
 CC INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND  
 CC FACTOR B TO ENZYMATICALLY ACTIVE C2A AND Bb AND THEREBY PREVENTS  
 CC THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVEYERS OF  
 CC THE COMPLEMENT CASCADE.  
 CC -1- FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED  
 CC VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).  
 CC -1- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT  
 CC HOMODIMER (MINOR FORM).  
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.  
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND  
 CC DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL  
 CC TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA COMPLEMENT  
 CC PROTEINS. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS  
 CC LINING EXTRACELLULAR COMPARTMENTS, AND VARIANTS OF THE MOLECULE  
 CC ARE PRESENT IN BODY FLUIDS AND IN EXTRACELLULAR MATRIX.  
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR THE  
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE  
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).  
 CC -1- PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.  
 CC -1- POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP  
 CC SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CR(A),  
 CC TC(A), DR(A), ES(A), WE(B), UMC, AND IFC) AND LOW-INCIDENCE  
 CC (TC(B), TC(C), AND WE(A)) ANTIGENS THAT RESIDE ON DAF. IN THE  
 CC CROMER PHENOTYPES DR(A-) AND INAB THERE IS REDUCED OR ABSENT  
 CC EXPRESSION OF DAF, RESPECTIVELY. IN THE CASE OF THE DR(A-) PHENOTYPE,  
 CC A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS  
 CC FOR TWO CHANGES: A SIMPLE AMINO ACID SUBSTITUTION THAT IS THE  
 CC BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING  
 CC EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS  
 CC PHENOTYPE.  
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.  
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION  
 CC (RCA) FAMILY.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD55 entry;  
 CC WWW-http://www.ncbi.nlm.nih.gov/prow/cd/cd55.htm".  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL: M31516; AAA52169.1; -;  
 DR EMBL: M30142; AAA52168.1; -;  
 DR EMBL: M15799; AAA52167.1; -;  
 DR EMBL: M64653; AAA52170.1; -;  
 DR EMBL: M64356; AAA52170.1; JOINED.  
 DR EMBL: S72858; AAC60633.1; -;  
 DR PIR: B26359; B26359;  
 DR PIR: A26359; A26359;  
 DR PIR: S16187; S16187;  
 DR PIR: A39101; A39101;  
 DR HSSP: S23138; S23138;  
 DR HSSP: P08603; 1HCC.  
 DR MIM: 125240; -;  
 DR INTERPRO: IPR000436; -;  
 DR PFAM: PF00084; sushi; 4.  
 KW Complement pathway; Plasma; Glycoprotein; Membrane; Repeat;  
 KM Alternative splicing; GPI-anchor; Signal; Sushi; Polymorphism;  
 KM Blood group antigen. 34  
 FT SIGNAL 1

FT CHAIN 35 353  
 FT PROPEP 354 381  
 FT DOMAIN 35 284  
 FT REPEAT 35 95  
 FT REPEAT 97 159  
 FT REPEAT 162 221  
 FT REPEAT 224 284  
 FT REPEAT 287 356  
 FT DOMAIN 287 356  
 FT DISULFID 65 94  
 FT DISULFID 98 145  
 FT DISULFID 129 158  
 FT DISULFID 163 204  
 FT DISULFID 190 220  
 FT DISULFID 225 267  
 FT DISULFID 253 283  
 FT CARBOHYD 95 95  
 FT LIPID 353 353  
 FT VARSPPLIC 362 381  
 FT  
 FT VARIANT 52 52  
 FT  
 FT VARIANT 52 52  
 FT  
 FT VARIANT 82 82  
 FT  
 FT VARIANT 199 199  
 FT  
 FT VARIANT 227 227  
 FT  
 FT CONFLICT 80 80  
 FT CONFLICT 85 85  
 FT  
 FT SEQUENCE 381 AA; 41388 MW; 29138EBB64B565E CRC64;  
 Query Match 37.0%; Score 408; DB 1; Length 381;  
 Best Local Similarity 42.6%; Pred. No. 2, 6e-30;  
 Matches 83; Conservative 29; Mismatches 69; Indels 14; Gaps 6;  
 QY 3 CNAPEMLPFA--RPTNLTDFEFPPIGYLNYECRPYSGSRF---STICLKNSTWGAKD 57  
 DB 98 CEVPTRLNSASLKOPYITTOY-PPVGIVAYEYECRPYGRPPSPKLTCLQNLKWSAYE 156  
 QY 58 RCRRRKSCNPDPVNGVHYIKIGIOGSOJKYSCTKGRYLIGSSAANCIIISGDTVIWNE 117  
 DB 157 FCKKSKCPNGEGELRNGIDVPGILFGCAITISFCGNCNGYKLFGSTSCLLSGSSVQWSDP 216  
 QY 118 TPLCDRIPLCGLPTPIANGDFTSISRETFHFGSVYTYHCNIGSGKKVFEIVGEPSTICTS 177  
 DB 217 LPFCRETYCPAPQIDINGIIG-ERDHYGYRQSYACNKG-----FTMIGHSIYCTV 269  
 QY 178 KDOVGIVSGPAPQC 192  
 DB 270 NNDE-GEWSGPPEPC 283  
 RESULT 5  
 DAF\_PONPY  
 ID DAF\_PONPY STANDARD; PRT; 340 AA.  
 AC P49457;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).  
 GN DAF OR CD55.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94110622; PubMed-7506731;  
 RA Nickells M.W., Alvarez J.I., Lublin D.M., Atkinson J.P.;



FT DISULFID 263 312 BY SIMILARITY.  
FT DISULFID 296 324 BY SIMILARITY.  
FT DISULFID 323 331 BY SIMILARITY.  
FT DISULFID 329 337 BY SIMILARITY.  
FT DISULFID 336 343 BY SIMILARITY.  
FT DISULFID 390 431 BY SIMILARITY.  
FT DISULFID 417 443 BY SIMILARITY.  
FT DISULFID 427 488 BY SIMILARITY.  
FT DISULFID 474 501 BY SIMILARITY.  
FT DISULFID 509 509 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).  
FT DISULFID 521 521 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).  
FT CARBOHYD 31 31 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 177 177 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 469 469 N-LINKED (GLCNAc. . .) (POTENTIAL).  
FT CARBOHYD 491 491 N-LINKED (GLCNAc. . .) (POTENTIAL).  
SO SEQUENCE 558 AA: 62266 MW: 59230667ED15EFF CRC64;

Query Match 33.6%; Score 370.5; DB 1; Length 558;  
Best Local Similarity 41.5%; Pred. No. 1,1e-26;  
Matches 80; Conservative 22; Mismatches 82; Indels 9; Gaps 3;

OY 2 OCNAPMLPAPPTNLDEEFPICITLYLVCECPGYS--GRPSIICLNKSVWTGAKDRG 59  
DB 14 KCGPPDLRYALPASEMNGTDESHITLXNCRPGYSRMSOSSLSICKPLGKMQ-INTAC 72  
OY 60 RRKSCNPPDPVNGVNVKIGIOFSGQIRYSCRGYRLIGSSATCIIISGDTYVWNEPP 119  
DB 73 VKKSCNPPDGLNGKVEKTDLFSGQIEFSCSEGYILIGSSITGYCEIOGKGVSWDPLP 132  
OY 120 ICDRIPCGAPITLNGDFTSISREYHGSVYTHHNLGSRKGVYELVGEPIYCTSKD 179  
DB 133 ECVIACGAPDISNKGHNGREEFYTRSSVYKCD-----PDFTLLGNASTICTYVN 186  
OY 180 DQVIGWSGAPOC 192  
DB 187 KTVGWSPSPPTC 199

RESULT 7  
DAF\_CAVPO STANDARD: PRT: 507 AA.  
ID Q60401; Q60402; Q60403; Q60404; Q60405; Q60406; P97254; P97255;  
AC P97256;  
DF 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE COMPLEMENT DECAV-ACCELERATING FACTOR PRECURSOR.  
GN DAF.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HARTLEY; TISSUE-SPLEEN;  
RX MEDLINE-95403978; PUBMED-7345710;  
RA Nonaka M., Miwa T., Okada N., Nonaka M., Okada H.;  
RT "Multiple isoforms of guinea pig decay-accelerating factor (DAF)  
generated by alternative splicing.";  
RT J. Immunol. 155:3037-3048(1995).  
RL J. Immunol. 155:3037-3048(1995).  
CC -I- FUNCTION: PREVENTS THE FORMATION AND/OR ACCELERATES THE  
DISOCIATION OF C3 CONVERTASE.  
CC -I- SUBCELLULAR LOCATION: CLASS GPI: ATTACHED TO THE MEMBRANE BY A  
GPI-ANCHOR.  
CC -I- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST SIX FORMS OF DAF  
TRANSCRIPTS (DISTRIBUTED IN FOUR CLASSES: GPI, TCL, TCS AND SEC)  
GENERATED BY ALTERNATIVE SPLICING. ONE GPI-ANCHORED FORM (GDAB-  
GPI), TWO FORMS WITH LONGER CYTOPLASMIC REGION (GDAB-TCL AND  
GDAB-TCS), TWO FORMS WITH SHORTER CYTOPLASMIC REGION (GDA-TCS AND  
GDA-TS) AND ONE SECRETED FORM (GDAB-SEC).  
CC -I- TISSUE SPECIFICITY: ALL THE ISOFORMS ARE WIDELY EXPRESSED. GPI AND  
TCS ARE THE MAJOR FORMS, WHEREAS SEC IS MINOR AND TCL IS ONLY

CC PRESENT IN TRACE LEVELS.  
CC -I- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS  
CC -I- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION  
(RCA) FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: D55667; BAA09514.1; JOINED.  
DR EMBL: D55656; BAA09514.1; JOINED.  
DR EMBL: D55657; BAA09514.1; JOINED.  
DR EMBL: D55658; BAA09514.1; JOINED.  
DR EMBL: D55659; BAA09514.1; JOINED.  
DR EMBL: D55660; BAA09514.1; JOINED.  
DR EMBL: D55661; BAA09514.1; JOINED.  
DR EMBL: D55662; BAA09514.1; JOINED.  
DR EMBL: D55663; BAA09514.1; JOINED.  
DR EMBL: D55664; BAA09514.1; JOINED.  
DR EMBL: D55665; BAA09514.1; JOINED.  
DR EMBL: D55666; BAA09514.1; JOINED.  
DR EMBL: D55667; BAA09514.1; JOINED.  
DR EMBL: D55668; BAA09514.1; JOINED.  
DR EMBL: D55669; BAA09514.1; JOINED.  
DR EMBL: D55670; BAA09514.1; JOINED.  
DR EMBL: D55671; BAA09514.1; JOINED.  
DR EMBL: D55672; BAA09514.1; JOINED.  
DR EMBL: D55673; BAA09514.1; JOINED.  
DR EMBL: D55674; BAA09514.1; JOINED.  
DR EMBL: D55675; BAA09514.1; JOINED.  
DR EMBL: D55676; BAA09514.1; JOINED.  
DR EMBL: D55677; BAA09514.1; JOINED.  
DR EMBL: D55678; BAA09514.1; JOINED.  
DR EMBL: D55679; BAA09514.1; JOINED.  
DR EMBL: D55680; BAA09514.1; JOINED.  
DR EMBL: D55681; BAA09514.1; JOINED.  
DR EMBL: D55682; BAA09514.1; JOINED.  
DR EMBL: D55683; BAA09514.1; JOINED.  
DR EMBL: D55684; BAA09514.1; JOINED.  
DR EMBL: D55685; BAA09514.1; JOINED.  
DR EMBL: D55686; BAA09514.1; JOINED.  
DR EMBL: D55687; BAA09514.1; JOINED.  
DR EMBL: D55688; BAA09514.1; JOINED.  
DR EMBL: D55689; BAA09514.1; JOINED.  
DR EMBL: D55690; BAA09514.1; JOINED.  
DR EMBL: D55691; BAA09514.1; JOINED.  
DR EMBL: D55692; BAA09514.1; JOINED.  
DR EMBL: D55693; BAA09514.1; JOINED.  
DR EMBL: D55694; BAA09514.1; JOINED.  
DR EMBL: D55695; BAA09514.1; JOINED.  
DR EMBL: D55696; BAA09514.1; JOINED.  
DR EMBL: D55697; BAA09514.1; JOINED.  
DR EMBL: D55698; BAA09514.1; JOINED.  
DR EMBL: D55699; BAA09514.1; JOINED.  
DR EMBL: D55700; BAA09514.1; JOINED.  
DR EMBL: D55701; BAA09514.1; JOINED.  
DR EMBL: D55702; BAA09514.1; JOINED.  
DR EMBL: D55703; BAA09514.1; JOINED.  
DR EMBL: D55704; BAA09514.1; JOINED.  
DR EMBL: D55705; BAA09514.1; JOINED.  
DR EMBL: D55706; BAA09514.1; JOINED.  
DR EMBL: D55707; BAA09514.1; JOINED.  
DR EMBL: D55708; BAA09514.1; JOINED.  
DR EMBL: D55709; BAA09514.1; JOINED.  
DR EMBL: D55710; BAA09514.1; JOINED.  
DR EMBL: D55711; BAA09514.1; JOINED.  
DR EMBL: D55712; BAA09514.1; JOINED.  
DR EMBL: D55713; BAA09514.1; JOINED.  
DR EMBL: D55714; BAA09514.1; JOINED.  
DR EMBL: D55715; BAA09514.1; JOINED.  
DR EMBL: D55716; BAA09514.1; JOINED.  
DR EMBL: D55717; BAA09514.1; JOINED.  
DR EMBL: D55718; BAA09514.1; JOINED.  
DR EMBL: D55719; BAA09514.1; JOINED.  
DR EMBL: D55720; BAA09514.1; JOINED.  
DR EMBL: D55721; BAA09514.1; JOINED.  
DR EMBL: D55722; BAA09514.1; JOINED.  
DR EMBL: D55723; BAA09514.1; JOINED.  
DR EMBL: D55724; BAA09514.1; JOINED.  
DR EMBL: D55725; BAA09514.1; JOINED.  
DR EMBL: D55726; BAA09514.1; JOINED.  
DR EMBL: D55727; BAA09514.1; JOINED.  
DR EMBL: D55728; BAA09514.1; JOINED.  
DR EMBL: D55729; BAA09514.1; JOINED.  
DR EMBL: D55730; BAA09514.1; JOINED.  
DR EMBL: D55731; BAA09514.1; JOINED.  
DR EMBL: D55732; BAA09514.1; JOINED.  
DR EMBL: D55733; BAA09514.1; JOINED.  
DR EMBL: D55734; BAA09514.1; JOINED.  
DR EMBL: D55735; BAA09514.1; JOINED.  
DR EMBL: D55736; BAA09514.1; JOINED.  
DR EMBL: D55737; BAA09514.1; JOINED.  
DR EMBL: D55738; BAA09514.1; JOINED.  
DR EMBL: D55739; BAA09514.1; JOINED.  
DR EMBL: D55740; BAA09514.1; JOINED.  
DR EMBL: D55741; BAA09514.1; JOINED.  
DR EMBL: D55742; BAA09514.1; JOINED.  
DR EMBL: D55743; BAA09514.1; JOINED.  
DR EMBL: D55744; BAA09514.1; JOINED.  
DR EMBL: D55745; BAA09514.1; JOINED.  
DR EMBL: D55746; BAA09514.1; JOINED.  
DR EMBL: D55747; BAA09514.1; JOINED.  
DR EMBL: D55748; BAA09514.1; JOINED.  
DR EMBL: D55749; BAA09514.1; JOINED.  
DR EMBL: D55750; BAA09514.1; JOINED.  
DR EMBL: D55751; BAA09514.1; JOINED.  
DR EMBL: D55752; BAA09514.1; JOINED.  
DR EMBL: D55753; BAA09514.1; JOINED.  
DR EMBL: D55754; BAA09514.1; JOINED.  
DR EMBL: D55755; BAA09514.1; JOINED.  
DR EMBL: D55756; BAA09514.1; JOINED.  
DR EMBL: D55757; BAA09514.1; JOINED.  
DR EMBL: D55758; BAA09514.1; JOINED.  
DR EMBL: D55759; BAA09514.1; JOINED.  
DR EMBL: D55760; BAA09514.1; JOINED.  
DR EMBL: D55761; BAA09514.1; JOINED.  
DR EMBL: D55762; BAA09514.1; JOINED.  
DR EMBL: D55763; BAA09514.1; JOINED.  
DR EMBL: D55764; BAA09514.1; JOINED.  
DR EMBL: D55765; BAA09514.1; JOINED.  
DR EMBL: D55766; BAA09514.1; JOINED.  
DR EMBL: D55767; BAA09514.1; JOINED.  
DR EMBL: D55768; BAA09514.1; JOINED.  
DR EMBL: D55769; BAA09514.1; JOINED.  
DR EMBL: D55770; BAA09514.1; JOINED.  
DR EMBL: D55771; BAA09514.1; JOINED.  
DR EMBL: D55772; BAA09514.1; JOINED.  
DR EMBL: D55773; BAA09514.1; JOINED.  
DR EMBL: D55774; BAA09514.1; JOINED.  
DR EMBL: D55775; BAA09514.1; JOINED.  
DR EMBL: D55776; BAA09514.1; JOINED.  
DR EMBL: D55777; BAA09514.1; JOINED.  
DR EMBL: D55778; BAA09514.1; JOINED.  
DR EMBL: D55779; BAA09514.1; JOINED.  
DR EMBL: D55780; BAA09514.1; JOINED.  
DR EMBL: D55781; BAA09514.1; JOINED.  
DR EMBL: D55782; BAA09514.1; JOINED.  
DR EMBL: D55783; BAA09514.1; JOINED.  
DR EMBL: D55784; BAA09514.1; JOINED.  
DR EMBL: D55785; BAA09514.1; JOINED.  
DR EMBL: D55786; BAA09514.1; JOINED.  
DR EMBL: D55787; BAA09514.1; JOINED.  
DR EMBL: D55788; BAA09514.1; JOINED.  
DR EMBL: D55789; BAA09514.1; JOINED.  
DR EMBL: D55790; BAA09514.1; JOINED.  
DR EMBL: D55791; BAA09514.1; JOINED.  
DR EMBL: D55792; BAA09514.1; JOINED.  
DR EMBL: D55793; BAA09514.1; JOINED.  
DR EMBL: D55794; BAA09514.1; JOINED.  
DR EMBL: D55795; BAA09514.1; JOINED.  
DR EMBL: D55796; BAA09514.1; JOINED.  
DR EMBL: D55797; BAA09514.1; JOINED.  
DR EMBL: D55798; BAA09514.1; JOINED.  
DR EMBL: D55799; BAA09514.1; JOINED.  
DR EMBL: D55800; BAA09514.1; JOINED.  
DR EMBL: D55801; BAA09514.1; JOINED.  
DR EMBL: D55802; BAA09514.1; JOINED.  
DR EMBL: D55803; BAA09514.1; JOINED.  
DR EMBL: D55804; BAA09514.1; JOINED.  
DR EMBL: D55805; BAA09514.1; JOINED.  
DR EMBL: D55806; BAA09514.1; JOINED.  
DR EMBL: D55807; BAA09514.1; JOINED.  
DR EMBL: D55808; BAA09514.1; JOINED.  
DR EMBL: D55809; BAA09514.1; JOINED.  
DR EMBL: D55810; BAA09514.1; JOINED.  
DR EMBL: D55811; BAA09514.1; JOINED.  
DR EMBL: D55812; BAA09514.1; JOINED.  
DR EMBL: D55813; BAA09514.1; JOINED.  
DR EMBL: D55814; BAA09514.1; JOINED.  
DR EMBL: D55815; BAA09514.1; JOINED.  
DR EMBL: D55816; BAA09514.1; JOINED.  
DR EMBL: D55817; BAA09514.1; JOINED.  
DR EMBL: D55818; BAA09514.1; JOINED.  
DR EMBL: D55819; BAA09514.1; JOINED.  
DR EMBL: D55820; BAA09514.1; JOINED.  
DR EMBL: D55821; BAA09514.1; JOINED.  
DR EMBL: D55822; BAA09514.1; JOINED.  
DR EMBL: D55823; BAA09514.1; JOINED.  
DR EMBL: D55824; BAA09514.1; JOINED.  
DR EMBL: D55825; BAA09514.1; JOINED.  
DR EMBL: D55826; BAA09514.1; JOINED.  
DR EMBL: D55827; BAA09514.1; JOINED.  
DR EMBL: D55828; BAA09514.1; JOINED.  
DR EMBL: D55829; BAA09514.1; JOINED.  
DR EMBL: D55830; BAA09514.1; JOINED.  
DR EMBL: D55831; BAA09514.1; JOINED.  
DR EMBL: D55832; BAA09514.1; JOINED.  
DR EMBL: D55833; BAA09514.1; JOINED.  
DR EMBL: D55834; BAA09514.1; JOINED.  
DR EMBL: D55835; BAA09514.1; JOINED.  
DR EMBL: D55836; BAA09514.1; JOINED.  
DR EMBL: D55837; BAA09514.1; JOINED.  
DR EMBL: D55838; BAA09514.1; JOINED.  
DR EMBL: D55839; BAA09514.1; JOINED.  
DR EMBL: D55840; BAA09514.1; JOINED.  
DR EMBL: D55841; BAA09514.1; JOINED.  
DR EMBL: D55842; BAA09514.1; JOINED.  
DR EMBL: D55843; BAA09514.1; JOINED.  
DR EMBL: D55844; BAA09514.1; JOINED.  
DR EMBL: D55845; BAA09514.1; JOINED.  
DR EMBL: D55846; BAA09514.1; JOINED.  
DR EMBL: D55847; BAA09514.1; JOINED.  
DR EMBL: D55848; BAA09514.1; JOINED.  
DR EMBL: D55849; BAA09514.1; JOINED.  
DR EMBL: D55850; BAA09514.1; JOINED.  
DR EMBL: D55851; BAA09514.1; JOINED.  
DR EMBL: D55852; BAA09514.1; JOINED.  
DR EMBL: D55853; BAA09514.1; JOINED.  
DR EMBL: D55854; BAA09514.1; JOINED.  
DR EMBL: D55855; BAA09514.1; JOINED.  
DR EMBL: D55856; BAA09514.1; JOINED.  
DR EMBL: D55857; BAA09514.1; JOINED.  
DR EMBL: D55858; BAA09514.1; JOINED.  
DR EMBL: D55859; BAA09514.1; JOINED.  
DR EMBL: D55860; BAA09514.1; JOINED.  
DR EMBL: D55861; BAA09514.1; JOINED.  
DR EMBL: D55862; BAA09514.1; JOINED.  
DR EMBL: D55863; BAA09514.1; JOINED.  
DR EMBL: D55864; BAA09514.1; JOINED.  
DR EMBL: D55865; BAA09514.1; JOINED.  
DR EMBL: D55866; BAA09514.1; JOINED.  
DR EMBL: D55867; BAA09514.1; JOINED.  
DR EMBL: D55868; BAA09514.1; JOINED.  
DR EMBL: D55869; BAA09514.1; JOINED.  
DR EMBL: D55870; BAA09514.1; JOINED.  
DR EMBL: D55871; BAA09514.1; JOINED.  
DR EMBL: D55872; BAA09514.1; JOINED.  
DR EMBL: D55873; BAA09514.1; JOINED.  
DR EMBL: D55874; BAA09514.1; JOINED.  
DR EMBL: D55875; BAA09514.1; JOINED.  
DR EMBL: D55876; BAA09514.1; JOINED.  
DR EMBL: D55877; BAA09514.1; JOINED.  
DR EMBL: D55878; BAA09514.1; JOINED.  
DR EMBL: D55879; BAA09514.1; JOINED.  
DR EMBL: D55880; BAA09514.1; JOINED.  
DR EMBL: D55881; BAA09514.1; JOINED.  
DR EMBL: D55882; BAA09514.1; JOINED.  
DR EMBL: D55883; BAA09514.1; JOINED.  
DR EMBL: D55884; BAA09514.1; JOINED.  
DR EMBL: D55885; BAA09514.1; JOINED.  
DR EMBL: D55886; BAA09514.1; JOINED.  
DR EMBL: D55887; BAA09514.1; JOINED.  
DR EMBL: D55888; BAA09514.1; JOINED.  
DR EMBL: D55889; BAA09514.1; JOINED.  
DR EMBL: D55890; BAA09514.1; JOINED.  
DR EMBL: D55891; BAA09514.1; JOINED.  
DR EMBL: D55892; BAA09514.1; JOINED.  
DR EMBL: D55893; BAA09514.1; JOINED.  
DR EMBL: D55894; BAA09514.1; JOINED.  
DR EMBL: D55895; BAA09514.1; JOINED.  
DR EMBL: D55896; BAA09514.1; JOINED.  
DR EMBL: D55897; BAA09514.1; JOINED.  
DR EMBL: D55898; BAA09514.1; JOINED.  
DR EMBL: D55899; BAA09514.1; JOINED.  
DR EMBL: D55900; BAA09514.1; JOINED.  
DR EMBL: D55901; BAA09514.1; JOINED.  
DR EMBL: D55902; BAA09514.1; JOINED.  
DR EMBL: D55903; BAA09514.1; JOINED.  
DR EMBL: D55904; BAA09514.1; JOINED.  
DR EMBL: D55905; BAA09514.1; JOINED.  
DR EMBL: D55906; BAA09514.1; JOINED.  
DR EMBL: D55907; BAA09514.1; JOINED.  
DR EMBL: D55908; BAA09514.1; JOINED.  
DR EMBL: D55909; BAA09514.1; JOINED.  
DR EMBL: D55910; BAA09514.1; JOINED.  
DR EMBL: D55911; BAA09514.1; JOINED.  
DR EMBL: D55912; BAA09514.1; JOINED.  
DR EMBL: D55913; BAA09514.1; JOINED.  
DR EMBL: D55914; BAA09514.1; JOINED.  
DR EMBL: D55915; BAA09514.1; JOINED.  
DR EMBL: D55916; BAA09514.1; JOINED.  
DR EMBL: D55917; BAA09514.1; JOINED.  
DR EMBL: D55918; BAA09514.1; JOINED.  
DR EMBL: D55919; BAA09514.1; JOINED.  
DR EMBL: D55920; BAA09514.1; JOINED.  
DR EMBL: D55921; BAA09514.1; JOINED.  
DR EMBL: D55922; BAA09514.1; JOINED.  
DR EMBL: D55923; BAA09514.1; JOINED.  
DR EMBL: D55924; BAA09514.1; JOINED.  
DR EMBL: D55925; BAA09514.1; JOINED.  
DR EMBL: D55926; BAA09514.1; JOINED.  
DR EMBL: D55927; BAA09514.1; JOINED.  
DR EMBL: D55928; BAA09514.1; JOINED.  
DR EMBL: D55929; BAA09514.1; JOINED.  
DR EMBL: D55930; BAA09514.1; JOINED.  
DR EMBL: D55931; BAA09514.1; JOINED.  
DR EMBL: D55932; BAA09514.1; JOINED.  
DR EMBL: D55933; BAA09514.1; JOINED.  
DR EMBL: D55934; BAA09514.1; JOINED.  
DR EMBL: D55935; BAA09514.1; JOINED.  
DR EMBL: D55936; BAA09514.1; JOINED.  
DR EMBL: D55937; BAA09514.1; JOINED.  
DR EMBL: D55938; BAA09514.1; JOINED.  
DR EMBL: D55939; BAA09514.1; JOINED.  
DR EMBL: D55940; BAA09514.1; JOINED.  
DR EMBL: D55941; BAA09514.1; JOINED.  
DR EMBL: D55942; BAA09514.1; JOINED.  
DR EMBL: D55943; BAA09514.1; JOINED.  
DR EMBL: D55944; BAA09514.1; JOINED.  
DR EMBL: D55945; BAA09514.1; JOINED.  
DR EMBL: D55946; BAA09514.1; JOINED.  
DR EMBL: D55947; BAA09514.1; JOINED.  
DR EMBL: D55948; BAA09514.1; JOINED.  
DR EMBL: D55949; BAA09514.1; JOINED.  
DR EMBL: D55950; BAA09514.1; JOINED.  
DR EMBL: D55951; BAA09514.1; JOINED.  
DR EMBL: D55952; BAA09514.1; JOINED.  
DR EMBL: D55953; BAA09514.1; JOINED.  
DR EMBL: D55954; BAA09514.1; JOINED.  
DR EMBL: D55955; BAA09514.1; JOINED.  
DR EMBL: D55956; BAA09514.1; JOINED.  
DR EMBL: D55957; BAA09514.1; JOINED.  
DR EMBL: D55958; BAA09514.1; JOINED.  
DR EMBL: D55959; BAA09514.1; JOINED.  
DR EMBL: D55960; BAA09514.1; JOINED.  
DR EMBL: D55961; BAA09514.1; JOINED.  
DR EMBL: D55962; BAA09514.1; JOINED.  
DR EMBL: D55963; BAA09514.1; JOINED.  
DR EMBL: D55964; BAA09514.1; JOINED.  
DR EMBL: D55965; BAA09514.1; JOINED.  
DR EMBL: D55966; BAA09514.1; JOINED.  
DR EMBL: D55967; BAA09514.1; JOINED.  
DR EMBL: D55968; BAA09514.1; JOINED.  
DR EMBL: D55969; BAA09514.1; JOINED.  
DR EMBL: D55970; BAA09514.1; JOINED.  
DR EMBL: D55971; BAA09514.1; JOINED.  
DR EMBL: D55972; BAA09514.1; JOINED.  
DR EMBL: D55973; BAA09514.1; JOINED.  
DR EMBL: D55974; BAA09514.1; JOINED.  
DR EMBL: D55975; BAA09514.1; JOINED.  
DR EMBL: D55976; BAA09514.1; JOINED.  
DR EMBL: D55977; BAA09514.1; JOINED.  
DR EMBL: D55978; BAA09514.1; JOINED.  
DR EMBL: D55979; BAA09514.1; JOINED.  
DR EMBL: D55980; BAA09514.1; JOINED.  
DR EMBL: D55981; BAA09514.1; JOINED.  
DR EMBL: D55982; BAA09514.1; JOINED.  
DR EMBL: D55983; BAA09514.1; JOINED.  
DR EMBL: D55984; BAA09514.1; JOINED.  
DR EMBL: D55985; BAA09514.1; JOINED.  
DR EMBL: D55986; BAA09514.1; JOINED.  
DR EMBL: D55987; BAA09514.1; JOINED.  
DR EMBL: D55988; BAA09514.1; JOINED.  
DR EMBL: D55989; BAA09514.1; JOINED.  
DR EMBL: D55990; BAA09514.1; JOINED.  
DR EMBL: D55991; BAA09514.1; JOINED.  
DR EMBL: D55992; BAA09514.1; JOINED.  
DR EMBL: D55993; BAA09514.1; JOINED.  
DR EMBL: D55994; BAA09514.1; JOINED.  
DR EMBL: D55995; BAA09514.1; JOINED.  
DR EMBL: D55996; BAA09514.1; JOINED.  
DR EMBL: D55997; BAA09514.1; JOINED.  
DR EMBL: D55998; BAA09514.1; JOINED.  
DR EMBL: D55999; BAA09514.1; JOINED.  
DR EMBL: D56000; BAA09514.1; JOINED.  
DR EMBL: D56001; BAA09514.1; JOINED.  
DR EMBL: D56002; BAA09514.1; JOINED.  
DR EMBL: D56003; BAA09514.1; JOINED.  
DR EMBL: D56004; BAA09514.1; JOINED.  
DR EMBL: D56005; BAA09514.1; JOINED.  
DR EMBL: D56006; BAA09514.1; JOINED.  
DR EMBL: D56007; BAA09514.1; JOINED.  
DR EMBL: D56008; BAA09514.1; JOINED.  
DR EMBL: D56009; BAA09514.1; JOINED.  
DR EMBL: D56010; BAA09514.1; JOINED.  
DR EMBL: D56011; BAA09514.1; JOINED.  
DR EMBL: D56012; BAA09514.1; JOINED.  
DR EMBL: D56013; BAA09514.1; JOINED.  
DR EMBL: D56014; BAA09514.1; JOINED.  
DR EMBL: D56015; BAA09514.1; JOINED.  
DR EMBL: D56016; BAA09514.1; JOINED.  
DR EMBL: D56017; BAA09514.1; JOINED.  
DR EMBL: D56018; BAA09514.1; JOINED.  
DR EMBL: D56019; BAA09514.1; JOINED.  
DR EMBL: D56020; BAA09514.1; JOINED.  
DR EMBL: D56021; BAA09514.1; JOINED.  
DR EMBL: D56022; BAA09514.1; JOINED.  
DR EMBL: D56023; BAA09514.1; JOINED.  
DR EMBL: D56024; BAA09514.1; JOINED.  
DR EMBL: D56025; BAA09514.1; JOINED.  
DR EMBL: D56026; BAA09514.1; JOINED.  
DR EMBL: D56027; BAA09514.1; JOINED.  
DR EMBL: D56028; BAA09514.1; JOINED.  
DR EMBL: D56029; BAA09514.1; JOINED.  
DR EMBL: D56030; BAA09514.1; JOINED.  
DR EMBL: D56031; BAA09514.1; JOINED.  
DR EMBL: D56032; BAA09514.1; JOINED.  
DR EMBL: D56033; BAA09514.1; JOINED.  
DR EMBL: D56034; BAA09514.1; JOINED.  
DR EMBL: D56035; BAA09514.1; JOINED.  
DR EMBL: D56036; BAA09514.1; JOINED.  
DR EMBL: D56037; BAA09514.1; JOINED.  
DR EMBL: D56038; BAA09514.1; JOINED.  
DR EMBL: D56039; BAA09514.1; JOINED.  
DR EMBL: D56040; BAA09514.1; JOINED.  
DR EMBL: D56041; BAA09514.1; JOINED.  
DR EMBL: D

[illegible]

OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC	Bovidae; Bovinae; Bos.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-LAYER:
RX	MEDLINE-95015909; PubMed-7930621;
RA	Hillarp A., Thern A., Dahlbaech B.;
RT	"Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains provides structural background for lack of complex formation with protein S";
RL	J. Immunol. 153:4190-4199(1994).
CC	-I- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BiNA), WHICH THEN HYDROLYSES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
CC	-I- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS (BY SIMILARITY).
CC	-I- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CC	-I- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; Z31693; CAA83498.1; .-
DR	HSSP; P10998; IYVC.
DR	INTERPRO; IPR000436; .-
DR	PfAM; PF00084; sushi; 8.
KM	Complement pathway; Plasma; Glycoprotein; Repeat; Sushi; Signal.
FT	SIGNAL 1 48 BY SIMILARITY.
FT	CHAIN 49 610 C4B-BINDING PROTEIN ALPHA CHAIN.
FT	DOMAIN 49 542 8 X SUSHI (SCR) REPEATS.
FT	REPEAT 49 108 SUSHI 1.
FT	REPEAT 111 170 SUSHI 2.
FT	REPEAT 173 235 SUSHI 3.
FT	REPEAT 238 295 SUSHI 4.
FT	REPEAT 298 363 SUSHI 5.
FT	REPEAT 366 426 SUSHI 6.
FT	REPEAT 428 484 SUSHI 7.
FT	REPEAT 486 542 SUSHI 8.
FT	DISULFID 50 95 BY SIMILARITY.
FT	DISULFID 80 107 BY SIMILARITY.
FT	DISULFID 112 153 BY SIMILARITY.
FT	DISULFID 139 169 BY SIMILARITY.
FT	DISULFID 174 217 BY SIMILARITY.
FT	DISULFID 203 234 BY SIMILARITY.
FT	DISULFID 239 281 BY SIMILARITY.
FT	DISULFID 267 294 BY SIMILARITY.
FT	DISULFID 299 350 BY SIMILARITY.
FT	DISULFID 334 362 BY SIMILARITY.
FT	DISULFID 7366 7390 BY SIMILARITY.
FT	DISULFID 7367 7412 BY SIMILARITY.
FT	DISULFID 7402 425 BY SIMILARITY.
FT	DISULFID 429 471 BY SIMILARITY.
FT	DISULFID 457 483 BY SIMILARITY.
FT	DISULFID 487 528 BY SIMILARITY.
FT	DISULFID 514 541 BY SIMILARITY.
FT	DISULFID 549 549 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT	DISULFID 561 561 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT	CARBOHYD 66 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD 221 221 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD 525 525 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD 602 602 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SEQ	SEQUENCE 610 AA; 68886 MW; D806B270E8A06B58 CnC64;

```

Query Match          33.0% Score 364.5; DB 1; Length 610;
Best Local Similarity 38.5% Pred. No. 4.1e-26;
Matches 74; Conservative 31; Mismatches 76; Indels 9; Gaps 3;

Oy 3 CNAFMPLPFARNTLTDEEFGITGLYLNNECPRGY--SGRPSPSICLKNSVTGAKDROR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 50 CGIPFYLDFAFPINFLNTRFETGTLRTCTCPGRISRRKRFLLICDGDGNKK-YKEFCV 108
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 RKSCRNPDPVNGVAVHVIKIGIQFGQIKSCATKGYRLIGSSATCIISGDIYIMDNEPPI 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 109 KKRCENPPELLNGVAYIVKTDYDFSGEIEFSCSEGYLLISANSYCOLQDKGVMSDPLPQ 168
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 121 CDRICGLPPTIANDDFISREYRHVGSVYVYHONLGSRGKAYELVGEBSYITCTSKDD 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 169 CIIACKEPPPTISNRHNGDEDFYTYGSSVYSCD-----RDFSMLGKASISCREVENK 222
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 181 QVGINSGPAPOC 192
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 TIGVMSPPSPSC 234
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
CR2_MOUSE STANDARD: PROT, 1025 AA.
ID CR2_MOUSE STANDARD: PROT, 1025 AA.
AC P19070:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 2, PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).
GN CR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=90229735; PubMed=2139457;
RA Fliegeroth J.D.;
RT "Comparative structure and evolution of murine CR2. The homolog of
   the human C3d/EBV receptor (CD21).";
RL J. Immunol. 144:3458-3467(1990).
[2]
RP SEQUENCE OF 12-1025 FROM N.A.
RX MEDLINE=91010789; PubMed=2145366;
RA Molina H., Kinoshita T., Inoue K., Carel J.C., Holers V.M.;
RT "A molecular and immunochemical characterization of mouse CR2.
   Evidence for a single gene model of mouse complement receptors 1 and
   2.";
RL J. Immunol. 145:2974-2983(1990).
[3]
RP SEQUENCE OF 343-401 AND 991-1025 FROM N.A.
RX MEDLINE=89098890; PubMed=2783485;
RA Fliegeroth J.D., Benedict M.A., Levy D.N., Strominger J.L.;
RT "Identification of murine complement receptor type 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:242-246(1989).
[4]
RP SEQUENCE OF 289-1025 FROM N.A.
RX MEDLINE=89381350; PubMed=2528587;
RA Kutzl C.B., Paul M.S., Aegeger M., Weis J.J., Weis J.H.;
RT "Murine complement receptor gene family. II. Identification and
   characterization of the murine homolog (cr2) to human CR2 and its
   molecular linkage to Cr2.";
RL J. Immunol. 143:2058-2067(1989).
[5]
RP FUNCTION: RECEPTOR FOR COMPLEMENT C3D. PARTICIPATES IN B
   LYMPHOCYTES ACTIVATION.
[6]
RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
[7]
RP TISSUE SPECIFICITY: B LYMPHOCYTES.
[8]
RP SIMILARITY: TO HUMAN C3D/EBV RECEPTOR (CD21).
[9]
RP SIMILARITY: CONTAINS 15 SUSHI (SCR) REPEATS.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

```

FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 694 694 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 790 790 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 813 813 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 851 851 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 901 901 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 289 291 YGS -> EFR (IN REF. 4).
FT CONFLICT 306 306 S -> T (IN REF. 2).
FT CONFLICT 520 520 P -> A (IN REF. 2).
FT CONFLICT 962 963 MISSING (IN REF. 4).
SQ SEQUENCE 1025 AA; 112994 MW; 19E51B9A0273694 CRC64;

Query Match 30.4%; Score 335.5; DB 1; Length 1025;
Best Local Similarity 33.9%; Pred. No. 3.3e-23;
Matches 74; Conservative 27; Mismatches 86; Indels 31; Gaps 6;

QY 3 CNAPE-WLPPFARPTNLDEFEFPY-----CTYINTECRPGY- 37
DB 124 CQANEMWPTLP--VCESDPLECPSPPTINGHHTGQHVDFVAGLSTVYSCPEYL 180
QY 38 -SGRPFSLICIKNSVMTGAKDRCKRSCNPPDPVNGVAVHIKIOFSGQIKSTCKYR 96
DB 181 LTGKK-TIKCIGSSGDMGVIFTCKEAGCEHRKFPNGVKREPLSLQVGTITVYFSCNEGY 239
QY 97 LIGSSAFCTIISGPTVIMDNFTPCDIRPCGLPTIANGDFTSISREYHYGVVTHCN 156
DB 240 LQGPSSQCVIEQKAIM-TKKPVCKELCPPPVRNNGSHGSENVPGYSTVYTCD 298
QY 157 LGSRGKVFELVGEPSYCTSKDOVGIWSPAPQCI 194
DB 299 PSEPKGVSTLIGKKTICTGSGQRTGIWSPAPYCVL 336

RESULT 10
C4BP_MOUSE STANDARD; PRT; 469 AA.
ID C4BP_MOUSE
AC P08607;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE C4B-BINDING PROTEIN PRECURSOR (C4BP).
GN CABPA OR C4BP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RX SEQUENCE FROM N.A. Pubmed=3663616.
RA Kristensen T., Ogata R.T., Chung L.P., Reid K.B.M., Tack B.F.;
RT "CDNA structure of murine C4b-binding protein, a regulatory component
RT of the serum complement system."
RL Biochemistry 26:4668-4674(1987).
CC -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
CC (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT
CC ALSO ACCELERATES THE DEGRADATION OF THE C4B2A COMPLEX (C3
CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA
CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
CC -1- SUBUNIT: HOMOPOLYMER; NOT COVALENTLY LINKED. MOUSE LACKS THE
CC BETA CHAIN OF C4BP.
CC -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M17122; AAA37312.1; ALT_INIT.
DR PIR; A27117; NEMSC4.
DR HSP; P10998; IYVC.
DR MGI; MGI:88229; C4BP.
DR INTERPRO; IPR000436; -.
DR PRAM; PR00084; Sush1; 6.
KW Complement pathway; Plasma; Glycoprotein; Repeat; Sush1; Signal.
FT SIGNAL 1
FT CHAIN 57 469 C4B-BINDING PROTEIN.
FT DOMAIN 57 414 6 X SUSHI (SCR) REPEATS.
FT REPEAT 57 116 SUSHI 1.
FT REPEAT 119 177 SUSHI 2.
FT REPEAT 180 241 SUSHI 3.
FT REPEAT 244 300 SUSHI 4.
FT REPEAT 302 356 SUSHI 5.
FT REPEAT 358 414 SUSHI 6.
FT DISULFID 58 103 BY SIMILARITY.
FT DISULFID 88 115 BY SIMILARITY.
FT DISULFID 120 160 BY SIMILARITY.
FT DISULFID 146 176 BY SIMILARITY.
FT DISULFID 181 223 BY SIMILARITY.
FT DISULFID 209 240 BY SIMILARITY.
FT DISULFID 245 287 BY SIMILARITY.
FT DISULFID 273 299 BY SIMILARITY.
FT DISULFID 303 343 BY SIMILARITY.
FT DISULFID 329 355 BY SIMILARITY.
FT DISULFID 359 400 BY SIMILARITY.
FT DISULFID 386 413 BY SIMILARITY.
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 469 AA; 51551 MW; 41E137C8BD6C6321 CRC64;

Query Match 29.5%; Score 325.5; DB 1; Length 469;
Best Local Similarity 37.1%; Pred. No. 1.2e-22;
Matches 72; Conservative 31; Mismatches 78; Indels 13; Gaps 6;

QY 2 CQNAPEWLPPFARPTNLDEFEFPYIGTYINTECRPGYSGRPS---IICKNSVMTGAKDR 58
DB 57 KCGPPALPNLPSADVVRITDESHRTLTLYECLDGY-GRGISRMVYCKPGEWE-ISVS 114
QY 59 CRRKSCRNPDPVNGVAVHIKIOFSGQIKSTCKYRLLIGSSSATCTIISGDTVIMDNET 118
DB 115 CAKHCRNPGLDNGYVNG-ETITFGSQTIESCOBGLFVSSSTSSCEVRKGVAMSNPF 173
QY 119 PICDIRPCGLPPTIANGDFTSISREYHYGVVTHCNLGSRGKRVDELVEPSIYCTSR 178
DB 174 PEYIVKRGPPDINSNGHSG-TEDFVYNNGISYTOPG-----FRLVGSFPIGCTIV 226
QY 179 DDQVGIWSPAPQC 192
DB 227 NKTVPVWSSSPPTC 240

RESULT 11
C4BP_HUMAN STANDARD; PRT; 597 AA.
ID C4BP_HUMAN
AC P04003;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

```



DE C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)  
 DE (PRP). OR C4BP.  
 GN C4BPA OR C4BP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LIVER;  
 RA MEDLINE-90073699; PubMed-2590215;  
 RA Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;  
 RT "Molecular cloning of the cDNA coding for proline-rich protein (PRP):  
 RT identity of PRP as C4b-binding protein.";  
 RL Biochem. Biophys. Res. Commun. 165:138-144(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91113199; PubMed-1989602;  
 RA Aso T., Okamura S., Matsuguchi T., Sakamoto N., Sata T., Niho Y.;  
 RT "Genomic organization of the alpha chain of the human C4b-binding  
 RT protein gene.";  
 RL Biochem. Biophys. Res. Commun. 174:222-227(1991).  
 RN [3]  
 RP SEQUENCE OF 9-81 FROM N.A.  
 RX MEDLINE-88242821; PubMed-3378624;  
 RA Lintin S.J., Lewin A.R., Reid K.B.M.;  
 RT "Derivation of the sequence of the signal peptide in human  
 RT C4b-binding protein and interspecies cross-hybridisation of the C4bp  
 RT cDNA sequence.";  
 RL FEBS Lett. 232:328-332(1988).  
 RN [4]  
 RP SEQUENCE OF 203-288 FROM N.A.  
 RX MEDLINE-86301119; PubMed-3017751;  
 RA Lintin S.J., Reid K.B.M.;  
 RT "Studies on the structure of the human C4b-binding protein gene.";  
 RL FEBS Lett. 204:77-81(1986).  
 RN [5]  
 RP SEQUENCE OF 80-597 FROM N.A.  
 RX MEDLINE-86025405; PubMed-3840370;  
 RA Chung L.P., Bentley D.R., Reid K.B.M.;  
 RT "Molecular cloning and characterization of the cDNA coding for C4b-  
 RT binding protein, a regulatory protein of the classical pathway of the  
 RT human complement system.";  
 RL Biochem. J. 230:133-141(1985).  
 RN [6]  
 RP SEQUENCE OF 49-88.  
 RX MEDLINE-85296001; PubMed-4033666;  
 RA Chung L.P., Gagnon J., Reid K.B.M.;  
 RT "Amino acid sequence studies of human C4b-binding protein: N-terminal  
 RT sequence analysis and alignment of the fragments produced by limited  
 RT proteolysis with chymotrypsin and the peptides produced by cyanogen  
 RT bromide treatment.";  
 RL Mol. Immunol. 22:427-435(1985).  
 RN [7]  
 RP ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, AND LIGAND BINDING.  
 RX MEDLINE-83221615; PubMed-6222381;  
 RA Dahlback B., Smith C.A., Mueller-Eberhard H.J.;  
 RT "Visualization of human C4b-binding protein and its complexes with  
 RT vitronectin K-dependent protein S and complement protein C2a.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).  
 CC -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT  
 CC ACTIVATION. IT BINDS AS A COFACTOR TO C3b/C4b INACTIVATOR  
 CC (C3bINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4b. IT  
 CC ALSO ACCELERATES THE DEGRADATION OF THE C4bC2a COMPLEX (C3  
 CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2a. ALPHA  
 CC CHAIN BINDS C4b. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S  
 CC AND WITH SERUM AMLOID P COMPONENT.  
 CC -1- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS  
 CC OF 3 POSSIBLE SORTS: A 570 KDA COMPLEX OF 7 ALPHA CHAINS AND 1  
 CC BETA CHAIN, A 530 KDA HOMOPOLYMER OF ALPHA CHAINS OR A 500 KDA  
 CC COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF  
 CC THE ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE  
 CC BINDING SITE FOR C4b AT THE END.  
 CC -1- TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.

CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.  
 CC -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOBOLIPROTEIN R.  
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M31452; AAA36507.1; -;  
 DR EMBL: M62486; AAA36506.1; -;  
 DR EMBL: M62475; AAA36506.1; JOINED.  
 DR EMBL: M62476; AAA36506.1; JOINED.  
 DR EMBL: M62477; AAA36506.1; JOINED.  
 DR EMBL: M62478; AAA36506.1; JOINED.  
 DR EMBL: M62479; AAA36506.1; JOINED.  
 DR EMBL: M62480; AAA36506.1; JOINED.  
 DR EMBL: M62481; AAA36506.1; JOINED.  
 DR EMBL: M62482; AAA36506.1; JOINED.  
 DR EMBL: M62484; AAA36506.1; JOINED.  
 DR EMBL: M62485; AAA36506.1; JOINED.  
 DR EMBL: X07853; CAA30701.1; -;  
 DR EMBL: X04284; CAA31244.1; -;  
 DR EMBL: X04296; CAA27839.1; -;  
 DR EMBL: X02865; CAA26617.1; -;  
 DR PIR: A33568; NBHUC4.  
 DR HSSP: P10998; LVVC.  
 DR MIM: 120830; -;  
 DR INTERPRO: IPR000436; -;  
 DR PFAM: PF00084; sushi; 8.  
 DR KW Complement pathway; Plasma; Glycoprotein; Repeat; Sushi; Signal;  
 DR Polymorphism.  
 KM  
 FT STGNAL 1 48  
 FT CHAIN 49 597  
 FT DOMAIN 49 539  
 FT REPEAT 49 109  
 FT REPEAT 112 171  
 FT REPEAT 174 235  
 FT REPEAT 238 295  
 FT REPEAT 298 361  
 FT REPEAT 364 423  
 FT REPEAT 425 481  
 FT REPEAT 483 539  
 FT DISULFID 50. 96  
 FT DISULFID 81. 108  
 FT DISULFID 113 154  
 FT DISULFID 140 170  
 FT DISULFID 175 217  
 FT DISULFID 203 234  
 FT DISULFID 239 281  
 FT DISULFID 267 294  
 FT DISULFID 299 348  
 FT DISULFID 332 360  
 FT DISULFID 7364 7387  
 FT DISULFID 7365 7409  
 FT DISULFID 7369 7422  
 FT DISULFID 426 468  
 FT DISULFID 454 480  
 FT DISULFID 484 525  
 FT DISULFID 511 538  
 FT DISULFID 546 546  
 FT DISULFID 558 558  
 FT CARBOHYD 221 221  
 FT CARBOHYD 506 506  
 FT CARBOHYD 528 528  
 FT CARBOHYD 92 92  
 FT VARIANT 357 357  
 FT SEQUENCE 597 AA; 67033 MM; 67E03FE2A85A10DD CRC64;  
 FT /FTID-VAR\_001978.  
 FT Y-> H.  
 FT Q-> T.  
 FT N-LINKED (GLCNAC. . .).  
 FT N-LINKED (GLCNAC. . .).  
 FT N-LINKED (GLCNAC. . .).  
 FT INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).  
 FT INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .).  
 FT N-LINKED (GLCNAC. . .).  
 FT Q-> T.  
 FT Y-> H.  
 FT /FTID-VAR\_001978.  
 FT 67E03FE2A85A10DD CRC64;

Qy	3	CNABEWLPFAPRTNLT-DEFEFPITGYLYNCECRPGY--SGRPFISICLKNSWTGARDRC	59
Qy	60	RRKSRNPDPVDYGNVHHYIKIGIQGSGQSKYKCTGKGYRLIGSSSATCIIISGDTYIWNDET	119
Dd	109	TYKRCHRGELRNNGVEYETKDTLSPSQSIQFSCSDEGFIISGTSRCEWQDRGVWSHPLP	166
Qy	120	ICDRIPCLPTPIANGDPTTISREYFHGYSVYVYHCNLGSGKGVFELVGEPSIYCTSKD	179
Dd	169	QCEIYKCKRPPDIRNGRRISG--EENYVANGFSVYTSCD-----PFFSLIGHASISCTAYEN	222
Qy	180	DQVGWISGPAPQC	192
Dd	222	ETIGVWRSPPTC	234
RESULT	12		
MCP_HUMAN			
ID	MCP_HUMAN	STANDARD:	PRT: 377 AA.
AC	P15529;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST		
DE	LEUCOCYTE COMMON ANTIGEN) (TLX).		
GN	MCP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 35-58.		
RA	MEDLINE=86286080; PubMed=3260937;		
RA	Lublin D.M., Liszewski M.K., Post T.W., Arce M.A., le Beau M.M.,		
RA	Rebentisch M.B., Lemons R.S., Seya T., Atkinson J.P.;		
RT	"Molecular cloning and chromosomal localization of human membrane		
RT	cofactor protein (MCP). Evidence for inclusion in the multigene		
RL	family of complement-regulatory proteins.",		
RL	J. Exp. Med. 168:181-194(1988).		
[2]			
RP	SEQUENCE FROM N.A.		
RC	TISSUE=TESTIS;		
RX	MEDLINE=93119658; PubMed=8418811;		
RA	Cervoni F., Fenichel P., Akhondji C., Hsi B.L., Rossi B.;		
RT	"Characterization of a cDNA clone coding for human testis membrane		
RT	cofactor protein (MCP, CD46)."		
RL	Mol. Reprod. Dev. 34:107-113(1993).		
[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.		
RX	MEDLINE=91267562; PubMed=2050389;		
RA	Purelli D.F., Russell S.M., Deacon N.J., Brown M.A., Hooker D.J.,		
RA	McKenzie I.F.,		
RT	"Alternatively spliced RNAs encode several isoforms of CD46 (MCP), a		
RT	regulator of complement activation."		
RL	Immunogenetics 33:335-344(1991).		
[4]			
RP	SEQUENCE OF 1-34 FROM N.A.		
RX	MEDLINE=94014356; PubMed=7691939;		
RA	Cui W., Horicade D., Post T., Greenlund A.C., Atkinson J.P.,		
RA	Kumar V.;		
RT	"Characterization of the promoter region of the membrane cofactor		
RT	protein (CD46) gene of the human complement system and comparison		
RT	to a membrane cofactor protein-like genetic element."		
RL	J. Immunol. 151:4137-4146(1993).		
[5]			
RP	ALTERNATIVE SPLICING.		
RX	MEDLINE=92289809; PubMed=1601037;		

[illegible]

```

FT VARSPLIC 286 300 MISSING (IN A SECOND FORM).
FT VARSPLIC 340 352 MISSING (IN ISOFORM M).
FT VARSPLIC 353 361 YLORRRKKG -> DIEFGRRKQWELMPLTRLNPIQ
FT VARSPLIC 362 377 QSRRAE (IN ISOFORM M).
FT VARSPLIC 362 377 TYLDETHREVEKFTSL -> KADGAEVATYQKSTTPAQ
FT VARSPLIC 362 377 RG (IN ISOFORM B/D/E/H/J/L).
FT VARSPLIC 362 377 MISSING (IN ISOFORM M AND ISOFORM N).
FT VARSPLIC 340 361 MISSING (IN ISOFORM N).
FT VARSPLIC 339 339 I -> IGKQWELMPLTRLNPIQOSRAE (IN
SO SEQUENCE 377 AA; 42247 MW; 2CA6F61752570B57 CRC64;
ISOFORM N).

Query Match 26.7%; Score 295; DB 1; Length 377;
Best Local Similarity 36.0%; Pred. No. 5.9e-20;
Matches 63; Conservative 25; Mismatches 77; Indels 10; Gaps 5;

QY 23 FPIGTLYNRCRPGYSGRP--FSIICLNKSWTC-AKDRCRKSCNPPDPVNGWHVI 78
DB 54 YELGERDYCKKGYFIPLPLATHTICDRNHTWLPVSDDACYKFCYIRDPNGQAVPA 113
QY 79 KG-IOFSSQIKYSCTKGKRYRLIGSSSACIISGDTVIMDNETPICDRIPCGLPPIANGDF 137
DB 114 NGTYEFYQWHEICNEGYLIGEEILYCELGSAVIMSGKPIECYKLCPPPKIKNGKH 173
QY 138 TTSIRREYFHGYSVTYHCNIGSRGKVFELVGPSTICTSKDOVGWISGAPQC 192
DB 174 TFEVEVEFYLDVATYSCD-PAPGPDPFSLIGESTIYCGDN---SVMSRAAPCC 223

RESULT 13
CCPH_HSVSA STANDARD; PRT; 360 AA.
ID CCPH_HSVSA 001016;
AC 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE COMPLEMENT CONTROL PROTEIN HOMOLOG PRECURSOR (CCPH).
GN 4 OR CCPH.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333688; PubMed=1321287;
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RL J. Virol. 66:5047-5058(1992).
RN [2]
RP SIMILARITY TO CCP.
RX MEDLINE=92260674; PubMed=1316492;
RA Albrecht J.-C., Fleckenstein B.;
RT "New member of the multigene family of complement control proteins in
herpesvirus saimiri.";
RL J. Virol. 66:3937-3940(1992).
CC -|- ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED FORM
CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
CC -|- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF
CC COMPLEMENT ACTIVATION (RCA).
CC -|- SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; X64346; CAA45626.1; -
DR EMBL; X64346; CAA45627.1; -

```

```

DR EMBL; X60283; CAA42823.1; -
DR EMBL; X60283; CAA42822.1; -
DR PIR; B42534; KMBE2E.
DR PIR; A42534; KMBE1E.
DR PIR; S24567; S24567.
DR HSSP; P10998; 1VVC.
DR INTERPRO; IPR000436; -
DR PRAM; PF00084; sushi; 4.
KW Signal; Repeat; Sushi; Transmembrane; Alternative splicing;
KW Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 360
FT DOMAIN 83 265
FT REPEAT 83 143
FT REPEAT 146 206
FT REPEAT 209 265
FT TRANSMEM 328 350
FT DISULFID 84 125
FT DISULFID 111 142
FT DISULFID 147 191
FT DISULFID 175 205
FT DISULFID 210 252
FT DISULFID 238 264
FT CARBOHYD 36 36
FT CARBOHYD 39 39
FT CARBOHYD 46 46
FT CARBOHYD 72 72
FT CARBOHYD 155 155
FT CARBOHYD 294 294
FT VARSPLIC 289 302
FT VARSPLIC 303 360
SO SEQUENCE 360 AA; 40006 MW; 6278A6C2ECD49669 CRC64;
MISSING (IN SHORT ISOFORM).

Query Match 26.4%; Score 292; DB 1; Length 360;
Best Local Similarity 36.1%; Pred. No. 1.1e-19;
Matches 66; Conservative 27; Mismatches 70; Indels 20; Gaps 7;

QY 16 NLTD-EPEFPIGTLYNRCRPGYSGRPFSIICLNKSWTGAKDRCRKRSCNPPDPVNGM 74
DB 36 NLTVSGPYNGTTLHTLHTCDEGAYAKRPVQVTCVNGWVYPK-KCQKKKSTPDDLNGR 94
QY 75 VHVIKIGFSSQIKYSCTKGKRYRLIGSSSACIIS-GDTVIMDNETPICDRIPCGLPPIA 133
DB 95 YTVAGNLYGVSIVTYTCNSGSLIGSTTACILKRGGRVDMTPPICDIKKCKPPOIA 154
QY 134 NGDPTTSIRREYFHGYSVTYHCNIGSRGKVFELVGPSTICTSKDOVGWISGAPQC 193
DB 155 NGHTNV-KDFYTYLDVATYSCN---DETKLTLTGPSKICS---ETGSM----- 197
QY 194 IPN 196
DB 198 VFN 200

RESULT 14
CR2_HUMAN STANDARD; PRT; 1033 AA.
ID CR2_HUMAN P20023;
AC P20023;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)
DE (EPSREIN-BARR VIRUS RECEPTOR) (CD21 ANTIGEN).
GN CR2 OR C3DR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89123277; PubMed=2563370;
RA Fujisaku A., Harley J.B., Frank M.B., Gruner B.A., Frazier B.,

```

[illegible]

Query Match	Best Local Similarity	Matches	75; Conservative	18; Mismatches	87; Indels	35; Gaps
QY 1 MOCNAP-EMLPFA-----RPTULTD-----EPEEPJIGTYNYECRPGY--SGRPF 42	26.3%; Score 290.5; DB 1; Length 1033;					
Db 301 IRCNAGTWEPAPVACEKECOAPRILNGOKEDRHMVFEFDGTSIKYCNPGYLVGEE- 449	34.9%; Pred. No. 4.4e-19;					
QY 43 STICLNKSVMTGAKDRCKRRKSCRN-----PDVVGAMVHVIKGIQFGSQIKYSCMKGYRL 97						
Db 450 SIQCSSEGVWTPRPVYQCKVACAEARGDULIKPQHOFRA-----PDVNSSCGEGFKL 501						
QY 98 IGGSSATCIIISGDYIWNENETPICDRIPCGEPLTIANGDFTSISREPHYSVYVYHCNL 157						
Db 502 SGSVYQEC---QGTLPMFMEIRLCKEITCPCPPPVYIYNAHIGSSLEDDPPTGYTVYTCNP 558						
QY 158 GSRGKKVFEIIVGEPISVYTSKDDQVIGMSGAPQC 192						

DB 559 GPERGVFSLIGESTIRCTSNDOERGTWSGPAPIC 593

RESULT 15

VCP\_VACCV STANDARD; PRT; 263 AA.

AC 010998:

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1988 (Rel. 11, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)

DE (PROTEIN C3) (28 KDA PROTEIN).

GN C3L.

OS Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OC [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.

RC STRAIN-WR:

RC MEDLINE=88318974; PubMed=3412473;

RA Kotwal G.J., Moss B.;

RT "Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";

RL Nature 335:176-178(1988).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN-WR:

RC MEDLINE=89073756; PubMed=2849238;

RA Kotwal G.J., Moss B.;

RT "Analysis of a large cluster of nonessential genes deleted from a vaccinia virus terminal transposition mutant.";

RL Virology 167:524-537(1988).

RL [3]

RP SEQUENCE FROM N.A.

RC STRAIN-COPENHAGEN:

RC MEDLINE=91021027; PubMed=2219722;

RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P., Paolletti E.;

RT "The complete DNA sequence of vaccinia virus.";

RL Virology 179:247-266(1990).

RL [4]

RP COMPLETE GENOME.

RC STRAIN-COPENHAGEN:

RC Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P., Paolletti E.;

RA Paolletti E.;

RL Virology 179:517-563(1990).

RL [5]

RP FUNCTION.

RC MEDLINE=92115714; PubMed=1731333;

RA Isaacs S.N., Kotwal G.J., Moss B.;

RT "Vaccinia virus complement-control protein prevents antibody-dependent complement-enhanced neutralization of infectivity and contributes to virulence.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).

RL [6]

RP STRUCTURE BY NMR OF 146-263.

RC MEDLINE=97446168; PubMed=9299352;

RA Wiles A.P., Shaw G., Bright J., Perczel A., Campbell I.D., Barlow P.N.;

RT "NMR studies of a viral protein that mimics the regulators of complement activation.";

RL J. Mol. Biol. 272:253-265(1997).

CC -I- FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

CC -I- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

CC -I- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/> or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).

CC -----

DR EMBL; X13166; CAA31564.1; -

DR EMBL; M22812; AAA69605.1; -

DR EMBL; M35027; AAA47997.1; -

DR PIR; A31005; WMVZSP.

DR PDB; 1VVC; 03-DEC-97.

DR PDB; 1VVD; 03-DEC-97.

DR PDB; 1VVE; 03-DEC-97.

DR INTERPRO: IPR000436; -

DR PFM; PF00084; sush1; 4

KW Signal; Repeat; Sush1; 3D-structure.

FT SIGNAL 1 19

FT CHAIN 20 263

FT DOMAIN 20 262

FT REPEAT 20 82

FT REPEAT 85 144

FT REPEAT 147 202

FT REPEAT 205 262

FT DISULFID 21 70

FT DISULFID 54 81

FT DISULFID 86 126

FT DISULFID 112 143

FT DISULFID 148 190

FT DISULFID 176 201

FT DISULFID 206 248

FT DISULFID 234 261

SO SEQUENCE 263 AA; 28629 MM; E4322CC9A6EF997 CRC64;

COMPLEMENT CONTROL PROTEIN.

4 X SUSHI (SCR) REPEATS.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

Query Match 26.1%; Score 288.5; DB 1; Length 263;

Best Local Similarity 35.0%; Pred. No. 1.6e-19;

Matches 71; Conservative 30; Mismatches 71; Indels 31; Gaps 11;

QY 3 CNAPEWLPFARPTNL-----TD-EFEPPIGTYLNECPREYSGRPFSLCLK--NSW 52

DB 21 CQTP-----SRPINKMKFNKSVETDANANNYIGDTLEYLCLPGRKQKMPYAKCTGTGW 75

QY 53 TGAKDRCRRKRCNPPDPVNGWVHVKIGFQSOIKYSCTKGKRLIGSSATCII--SGDT 111

DB 76 T-LFNOCIRKRPSPRDINDGOLD-IGGVDFGSSITSCNSGHLIGESKSTCELASTGS 133

QY 112 VIWDMETPICDRIPGCLPTIANGDFTSISREYFHGSVVYVHCNLSGRKVFELWGP 171

DB 134 MVMNPEAPICSEVKQSPSISNGRHNGY-EDFYTGDSVVTYSCNSG-----YSLIGNS 186

QY 172 STYCTSKDQVGIVSGPAPQCII 194

DB 187 GVLCSG-----GEWSDP-PTCOI 203

Search completed: January 13, 2001, 13:47:40

UO time: 385 sec

**THIS PAGE BLANK (USPTO)**

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: January 13, 2001, 13:42:36 ; Search time 73.65 Seconds  
(Without alignments)  
313.509 Million cell updates/sec

Title: US-09-380-682-1  
Perfect score: 1104  
Sequence: 1 MGNAPWLPFARPTNLDE.....KDDQVGTWSPAPCIIIPNK 197

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_PISC:\*  
8: SP\_ORNITHINE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	94.4	559	4 Q9UOV2	Q9UOV2 homo sapien
2	1042	94.4	2039	4 Q16745	Q16745 homo sapien
3	1042	94.4	2489	4 Q16744	Q16744 homo sapien
4	1029	93.2	661	6 Q29531	Q29531 pan troglod
5	1029	93.2	2014	6 Q29530	Q29530 pan troglod
6	946	85.7	522	6 Q28769	Q28769 papio hamad
7	937	84.9	522	6 Q28797	Q28797 pan troglod
8	923	83.6	315	6 Q28770	Q28770 papio hamad
9	780	70.7	1911	6 Q29528	Q29528 papio hamad
10	702	63.6	483	11 Q64735	Q64735 mus musculu
11	689	62.4	497	11 Q63612	Q63612 rattus norv
12	689	62.4	559	11 Q63135	Q63135 rattus norv
13	681	61.7	162	4 Q9UOR7	Q9UOR7 homo sapien
14	624	56.5	679	11 Q99254	Q99254 mus musculu
15	474	42.9	330	11 Q62479	Q62479 mus musculu
16	433	37.4	343	6 Q9MYJ3	Q9MYJ3 macaca mula
17	410	37.1	305	6 Q9MYJ5	Q9MYJ5 pan troglod
18	410	37.1	347	6 Q9MYJ6	Q9MYJ6 pan troglod
19	409	37.0	347	6 Q9MYJ7	Q9MYJ7 gorilla gor

20	407	36.9	347	4 P78361	P78361 homo sapien
21	406	36.8	271	6 Q9MYJ0	Q9MYJ0 erythrocebu
22	406	36.8	278	6 Q9MYJ1	Q9MYJ1 erythrocebu
23	406	36.8	343	6 Q9MYJ2	Q9MYJ2 erythrocebu
24	406	36.8	343	6 Q9MYJ2	Q9MYJ2 erythrocebu
25	405	36.7	343	6 Q9MYJ4	Q9MYJ4 papio hamad
26	399	36.1	257	11 Q61447	Q61447 mus musculu
27	375	34.0	363	6 Q02839	Q02839 sus scrofa
28	366	33.2	180	11 Q60400	Q60400 cavia porce
29	364.5	33.0	383	11 Q9WT19	Q9WT19 cavia porce
30	363	32.9	372	11 Q9QYJ9	Q9QYJ9 rattus norv
31	363	32.9	382	11 Q9QUT3	Q9QUT3 rattus norv
32	363	32.9	399	11 Q9QUM0	Q9QUM0 rattus norv
33	363	32.9	399	11 Q9QUM6	Q9QUM6 rattus norv
34	363	32.9	466	11 Q92019	Q92019 rattus norv
35	353	32.0	417	11 Q35520	Q35520 rattus norv
36	353	32.0	533	11 Q08569	Q08569 cavia porce
37	344	31.2	89	11 Q63129	Q63129 rattus norv
38	342.5	31.0	579	11 Q60736	Q60736 mus musculu
39	311	28.2	645	12 Q9WRU2	Q9WRU2 macaca mula
40	306	27.7	1045	6 Q46545	Q46545 ovls aries
41	299.5	27.1	377	6 Q62838	Q62838 saguinus oe
42	299.5	27.1	378	6 Q62837	Q62837 saguinus oe
43	295	26.7	349	4 Q15429	Q15429 homo sapien
44	293.5	26.6	395	12 Q9J2M6	Q9J2M6 macaca mula
45	292.5	26.5	285	6 Q19121	Q19121 papio hamad

## ALIGNMENTS

```

RESULT 1
ID Q9UOV2 PRELIMINARY; PRT; 559 AA.
AC Q9UOV2;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE HUMAN CRI MRNA FOR C3B/C4B RECEPTOR SECRETED FORM PRECURSOR
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=89010527; Pubmed=2971757;
RA Hourcade D., Miesner D.R., Atkinson J.P., Hoiers V.M.;
RT Identification of an alternative polyadenylation site in the human
RT C3b/C4b receptor (complement receptor type 1) transcriptional unit and
RT prediction of a secreted form of complement receptor type 1.
RL J. Exp. Med. 168:1255-1270(1988).
DR EMBL: X14362; CAA32541.1;
DR HSSP: P10998; 1VVD.
DR INTERPRO: IPR000436;
DR INTERPRO: IPR000834;
DR INTERPRO: IPR002396;
DR PIRAM: PF00084; sushi; 8.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
KW SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 16 POTENTIAL.
FT CHAIN 17 559 POTENTIAL.
SO SEQUENCE 559 AA; 61424 MW; DBFPE955CA179D75 CRC64;

```

Query Match 94.4%; Score 1042; DB 4; Length 559;  
Best Local Similarity 94.9%; Pred. No. 9.7e-101;  
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```
Db 17 QCNAPWLPFARPTNLDEFEFFPIGTLYNTECRPGYSGRPSIICLNKSVTGAKDRCR 76
QY 62 KSCRNPDPVNGMVHVIGIOFGSQIKYKSCYRLLIGSSSATCIIISGDTYIMDNEPIC 121
Db 77 KSCRNPDPVNGMVHVIGIOFGSQIKYKSCYRLLIGSSSATCIIISGDTYIMDNEPIC 136
QY 122 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 181
Db 137 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 196
QY 182 VGWISGPAPQCIIPNK 197
Db 197 VGWISGPAPQCIIPNK 212

RESULT 2
Q16745 PRELIMINARY: PRT: 2039 AA.
ID 016745
AC 016745.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COMPLEMENT RECEPTOR 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94065175; PubMed=8245463;
RA Vik D.P., Wong W.W.;
RT "Structure of the gene for the F allele of complement receptor type 1
RL J. Immunol. 151:6214-6224(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Vik D.P., Wong W.W.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL, L17418; AAB60694.1; JOINED.
DR EMBL, L17390; AAB60694.1; JOINED.
DR EMBL, L17391; AAB60694.1; JOINED.
DR EMBL, L17392; AAB60694.1; JOINED.
DR EMBL, L17393; AAB60694.1; JOINED.
DR EMBL, L17394; AAB60694.1; JOINED.
DR EMBL, L17395; AAB60694.1; JOINED.
DR EMBL, L17396; AAB60694.1; JOINED.
DR EMBL, L17397; AAB60694.1; JOINED.
DR EMBL, L17398; AAB60694.1; JOINED.
DR EMBL, L17399; AAB60694.1; JOINED.
DR EMBL, L17400; AAB60694.1; JOINED.
DR EMBL, L17401; AAB60694.1; JOINED.
DR EMBL, L17402; AAB60694.1; JOINED.
DR EMBL, L17403; AAB60694.1; JOINED.
DR EMBL, L17404; AAB60694.1; JOINED.
DR EMBL, L17405; AAB60694.1; JOINED.
DR EMBL, L17406; AAB60694.1; JOINED.
DR EMBL, L17407; AAB60694.1; JOINED.
DR EMBL, L17408; AAB60694.1; JOINED.
DR EMBL, L17409; AAB60694.1; JOINED.
DR EMBL, L17410; AAB60694.1; JOINED.
DR EMBL, L17411; AAB60694.1; JOINED.
DR EMBL, L17412; AAB60694.1; JOINED.
DR EMBL, L17413; AAB60694.1; JOINED.
DR EMBL, L17414; AAB60694.1; JOINED.
DR EMBL, L17415; AAB60694.1; JOINED.
DR EMBL, L17416; AAB60694.1; JOINED.
DR EMBL, L17417; AAB60694.1; JOINED.
DR EMBL, L17419; AAB60694.1; JOINED.
DR EMBL, L17420; AAB60694.1; JOINED.
DR EMBL, L17421; AAB60694.1; JOINED.
DR EMBL, L17422; AAB60694.1; JOINED.
DR EMBL, L17423; AAB60694.1; JOINED.
HSP; P08603; IHLI.
```

```
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000834; -.
DR INTERPRO: IPR001424; -.
DR PFAM: PF00084; sushi; 30.
DR PROSITE: PS00087; SOD_CU_ZN_1; UNKNOWN_1.
DR PROSITE: PS00133; CARBOXYEPT_ZN_2; UNKNOWN_2.
SQ SEQUENCE 2039 AA; 223603 MW; B82FCB1106B16635 CRC64;

Query Match 94.4%; Score 1042; DB 4; Length 2039;
Best Local Similarity 94.9%; Pred. No. 4.8e-100;
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLDEFEFFPIGTLYNTECRPGYSGRPSIICLNKSVTGAKDRCR 61
Db 42 QCNAPWLPFARPTNLDEFEFFPIGTLYNTECRPGYSGRPSIICLNKSVTGAKDRCR 101
QY 62 KSCRNPDPVNGMVHVIGIOFGSQIKYKSCYRLLIGSSSATCIIISGDTYIMDNEPIC 121
Db 102 KSCRNPDPVNGMVHVIGIOFGSQIKYKSCYRLLIGSSSATCIIISGDTYIMDNEPIC 161
QY 122 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 181
Db 162 DRIPGGLPPTIANGDFTSISREYFHGYSVVTYHGNLGSRGKRVFELVGEPSIYCTSKDDQ 221
QY 182 VGWISGPAPQCIIPNK 197
Db 222 VGWISGPAPQCIIPNK 237

RESULT 3
Q16744 PRELIMINARY: PRT: 2489 AA.
ID 016744
AC 016744.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COMPLEMENT RECEPTOR 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94065175; PubMed=8245463;
RA Vik D.P., Wong W.W.;
RT "Structure of the gene for the F allele of complement receptor type 1
RL J. Immunol. 151:6214-6224(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Vik D.P., Wong W.W.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL, L17418; AAB60695.1; JOINED.
DR EMBL, L17390; AAB60695.1; JOINED.
DR EMBL, L17391; AAB60695.1; JOINED.
DR EMBL, L17392; AAB60695.1; JOINED.
DR EMBL, L17393; AAB60695.1; JOINED.
DR EMBL, L17394; AAB60695.1; JOINED.
DR EMBL, L17395; AAB60695.1; JOINED.
DR EMBL, L17396; AAB60695.1; JOINED.
DR EMBL, L17397; AAB60695.1; JOINED.
DR EMBL, L17398; AAB60695.1; JOINED.
DR EMBL, L17399; AAB60695.1; JOINED.
DR EMBL, L17400; AAB60695.1; JOINED.
DR EMBL, L17401; AAB60695.1; JOINED.
DR EMBL, L17402; AAB60695.1; JOINED.
DR EMBL, L17403; AAB60695.1; JOINED.
DR EMBL, L17404; AAB60695.1; JOINED.
DR EMBL, L17405; AAB60695.1; JOINED.
DR EMBL, L17406; AAB60695.1; JOINED.
DR EMBL, L17407; AAB60695.1; JOINED.
DR EMBL, L17408; AAB60695.1; JOINED.
DR EMBL, L17409; AAB60695.1; JOINED.
```



DR EMBL: L17410: AAB60695.1; JOINED.  
DR EMBL: L17411: AAB60695.1; JOINED.  
DR EMBL: L17412: AAB60695.1; JOINED.  
DR EMBL: L17413: AAB60695.1; JOINED.  
DR EMBL: L17414: AAB60695.1; JOINED.  
DR EMBL: L17415: AAB60695.1; JOINED.  
DR EMBL: L17416: AAB60695.1; JOINED.  
DR EMBL: L17417: AAB60695.1; JOINED.  
DR EMBL: L17418: AAB60695.1; JOINED.  
DR EMBL: L17419: AAB60695.1; JOINED.  
DR EMBL: L17420: AAB60695.1; JOINED.  
DR EMBL: L17421: AAB60695.1; JOINED.  
DR EMBL: L17422: AAB60695.1; JOINED.  
DR EMBL: L17423: AAB60695.1; JOINED.  
DR EMBL: L17424: AAB60695.1; JOINED.  
DR EMBL: L17425: AAB60695.1; JOINED.  
DR EMBL: L17426: AAB60695.1; JOINED.  
DR EMBL: L17427: AAB60695.1; JOINED.  
DR EMBL: L17428: AAB60695.1; JOINED.  
DR EMBL: L17429: AAB60695.1; JOINED.  
DR EMBL: L17430: AAB60695.1; JOINED.  
DR HSP: P08603; 1HFI.  
DR INTERPRO: IPR000436; -.  
DR INTERPRO: IPR000834; -.  
DR INTERPRO: IPR001424; -.  
DR PFAM: PF00084; sush1; 37.  
DR PROSITE: PS00087; SOD\_CU\_ZN\_1; UNKNOWN\_1.  
DR PROSITE: PS00133; CARBOXYPEPT\_ZN\_2; UNKNOWN\_3.  
SQ SEQUENCE 2489 AA; 272846 MW; CEE1B53F2B4FAF6 CRC64;

Query Match 94.4%; Score 1042; DB 4; Length 2489;  
Best Local Similarity 94.9%; Pred. No. 6.1e-100;  
Matches 186; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QCNAPEWLPFARPTNLDEFEFFIGTYLNECRPGYSGRPSIICLNKSVTGAKDCRR 61  
DB 42 QCNAPEWLPFARPTNLDEFEFFIGTYLNECRPGYSGRPSIICLNKSVTGAKDCRR 101  
QY 62 KSCNPPDPVNGMVHYKIGIOFGSQIKYSGTKGRLIGSSATCIIISGDVYIMNEPPI 121  
DB 102 KSCNPPDPVNGMVHYKIGIOFGSQIKYSGTKGRLIGSSATCIIISGDVYIMNEPPI 161  
QY 122 DRIPCGLPPTITNGDFISTNRENFHYGSVYTHCNLSRGKRVELGEPSTYCTSDQ 181  
DB 162 DRIPCGLPPTITNGDFISTNRENFHYGSVYTHCNLSRGKRVELGEPSTYCTSDQ 221  
QY 182 VGIMSGAPQCIIPNK 197  
DB 222 VGIMSGAPQCIIPNK 237

RESULT 4  
Q29531 PRELIMINARY; PRT; 661 AA.  
AC Q29531:  
DT 01-NOV-1996 (TEMBLrel. 01, Created)  
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
DE 01-OCT-2000 (TEMBLrel. 15, Last annotation update)  
DE COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).  
GN CRI.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94292799; PubMed=8021505;  
RA Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;  
RT "Primary sequence of an alternatively spliced form of CRI. Candidate  
RT for the 75,000 M(r) complement receptor expressed on chimpanzee  
RT erythrocytes.";  
RL J. Immunol. 153:691-700(1994).  
DR EMBL: L24921; AAA51439.1; -.  
DR

DR HSP: P10998; 1VVD.  
DR INTERPRO: IPR000436; -.  
DR INTERPRO: IPR001424; -.  
DR INTERPRO: IPR002396; -.  
DR PFAM: PF00084; sush1; 9.  
DR PRINTS: PR00343; SELECTIN.  
DR PROSITE: PS00087; SOD\_CU\_ZN\_1; UNKNOWN\_1.  
KW Signal; Alternative splicing.  
FT NON\_TER 1  
FT SIGNAL 1  
FT CHAIN <1 16  
FT NON\_TER 17 >661  
FT NON\_TER 661  
SQ SEQUENCE 661 AA; 72966 MW; 3F0DF1532664D3F0 CRC64;

Query Match 93.2%; Score 1029; DB 6; Length 661;  
Best Local Similarity 93.9%; Pred. No. 2.7e-99;  
Matches 184; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 QCNAPEWLPFARPTNLDEFEFFIGTYLNECRPGYSGRPSIICLNKSVTGAKDCRR 61  
DB 17 QCNAPEWLPFARPTNLDEFEFFIGTYLNECRPGYSGRPSIICLNKSVTGAKDCRR 76  
QY 62 KSCNPPDPVNGMVHYKIGIOFGSQIKYSGTKGRLIGSSATCIIISGDVYIMNEPPI 121  
DB 77 KSCNPPDPVNGMVHYKIGIOFGSQIKYSGTKGRLIGSSATCIIISGDVYIMNEPPI 136  
QY 122 DRIPCGLPPTITNGDFISTNRENFHYGSVYTHCNLSRGKRVELGEPSTYCTSDQ 181  
DB 137 DRIPCGLPPTITNGDFISTNRENFHYGSVYTHCNLSRGKRVELGEPSTYCTSDQ 196  
QY 182 VGIMSGAPQCIIPNK 197  
DB 197 VGIMSGAPQCIIPNK 212

RESULT 5  
Q29530 PRELIMINARY; PRT; 2014 AA.  
AC Q29530:  
DT 01-NOV-1996 (TEMBLrel. 01, Created)  
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
DE 01-MAY-2000 (TEMBLrel. 13, Last annotation update)  
DE COMPLEMENT RECEPTOR 1 (FRAGMENT).  
GN CRI.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94292799; PubMed=8021505;  
RA Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;  
RT "Primary sequence of an alternatively spliced form of CRI. Candidate  
RT for the 75,000 M(r) complement receptor expressed on chimpanzee  
RT erythrocytes.";  
RL J. Immunol. 153:691-700(1994).  
DR EMBL: L24920; AAA51438.1; -.  
DR HSP: P08603; 1HFI.  
DR INTERPRO: IPR000436; -.  
DR INTERPRO: IPR000834; -.  
DR INTERPRO: IPR001424; -.  
DR PFAM: PF00084; sush1; 30.  
DR PROSITE: PS00087; SOD\_CU\_ZN\_1; UNKNOWN\_1.  
DR PROSITE: PS00133; CARBOXYPEPT\_ZN\_2; UNKNOWN\_2.  
FT NON\_TER 1  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 2014 AA; 221280 MW; 6D6C3A74D81F1DB9 CRC64;

Query Match 93.2%; Score 1029; DB 6; Length 2014;  
Best Local Similarity 93.9%; Pred. No. 1.1e-98;  
Matches 184; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

```

QY 2 QCNAPWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIITCLKNSVWTGAKDRCR 61
D 17 QCNAPWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIITCLKNSVWTGAKDRCR 76
QY 62 KSCRNPDPVNGMVAVYKIGIOGSOIKYSCRTGKYLIGSSSATCIIISGDTYIWDNETPIC 121
D 77 KSCRNPDPVNGMVAVYKIGIOGSOIKYSCRTGKYLIGSSSATCIIISGDTYIWDNETPIC 136
QY 122 DRIPGCLPTTANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 181
D 137 DRIPGCLPTTANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 196
QY 182 VGIWSPAPQCIIPNK 197
D 197 VGIWSPAPQCIIPNK 212

RESULT 6
Q28769 PRELIMINARY; PRT; 522 AA.
AC Q28769:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE COMPLEMENT RECEPTOR (FRAGMENT).
OS Papilio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Birmingham D.J., Logar C.M., Shen X.P., Chen W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L77977; AAA99004.1; -.
DR HSSP: P10998; 1YVD.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00084; sush1; 7.
DR PRINTS: PR00343; SELECTIN.
FT NON_TER 1
FT SEQUENCE 522 AA; 56626 MW; 312FCBE03ADF19DC CRC64;

Query Match
Best Local Similarity 85.7%; Score 946; DB 6; Length 522;
Matches 171; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 2 QCNAPWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIITCLKNSVWTGAKDRCR 61
D 47 QCNAPWLPFARPTNLTDEFEPPITGYLYNECRPGYSGRPSIITCLKNSVWTGAKDRCR 106
QY 62 KSCRNPDPVNGMVAVYKIGIOGSOIKYSCRTGKYLIGSSSATCIIISGDTYIWDNETPIC 121
D 107 KSCRNPDPVNGMVAVYKIGIOGSOIKYSCRTGKYLIGSSSATCIIISGDTYIWDNETPIC 166
QY 122 DRIPGCLPTTANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 181
D 167 DRIPGCLPTTANGDFTSISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQ 226
QY 182 VGIWSPAPQCIIPNK 197
D 227 VGIWSPAPQCIIPNK 242

RESULT 7
Q28797 PRELIMINARY; PRT; 522 AA.
AC Q28797:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

```

```

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE UNKNOWN PROTEIN (FRAGMENT).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292799; PubMed=8021505;
RA Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;
RT "Primary sequence of an alternatively spliced form of CR1. Candidate
RT for the 75,000 M(r) complement receptor expressed on chimpanzee
RT erythrocytes."
RL J. Immunol. 153:691-700(1994).
DR EMBL: L24922; AAA50460.1; -.
DR HSSP: P10998; 1YVD.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000834; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00084; sush1; 8.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00133; CARBOXYDEPT_2N_2; UNKNOWN_1.
FT NON_TER 1
FT SEQUENCE 522 AA; 57304 MW; DB8456EF462C00C9 CRC64;

Query Match
Best Local Similarity 84.9%; Score 937; DB 6; Length 522;
Matches 167; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 19 DEFEPPITGYLYNECRPGYSGRPSIITCLKNSVWTGAKDRCRKSCRNPDPVNGMVAVI 78
D 1 DEFEPPITGYLYNECRPGYSGRPSIITCLKNSVWTGAKDRCRKSCRNPDPVNGMVAVI 60
QY 79 KIGIOGSOIKYSCRTGKYLIGSSSATCIIISGDTYIWDNETPICRIPGCLPTTANGDFT 138
D 61 KIGIOGSOIKYSCRTGKYLIGSSSATCIIISGDTYIWDNETPICRIPGCLPTTANGDFT 120
QY 139 SISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQYGIWSPAPQCIIPNK 197
D 121 SISREYFHGVSVTYHCNLSGRKKVFEIYGEPSIYCTSKDDQYGIWSPAPQCIIPNK 179

RESULT 8
Q28770 PRELIMINARY; PRT; 315 AA.
AC Q28770:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE COMPLEMENT RECEPTOR (FRAGMENT).
OS Papilio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Birmingham D.J., Logar C.M., Shen X.P., Chen W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L77978; AAA99005.1; -.
DR HSSP: P10998; 1YVD.
DR INTERPRO: IPR000436; -.
DR PFAM: PF00084; sush1; 5.
FT NON_TER 1
FT SEQUENCE 315 AA; 35172 MW; 305B314AE752824F CRC64;

Query Match
Best Local Similarity 83.6%; Score 923; DB 6; Length 315;
Matches 166; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

```

```

OY 2 OCNAPBFLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 61
    1 QCNAPBFLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 60
DB 1 QCNAPBFLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 60
OY 62 KSCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 121
    61 KSCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 120
DB 122 DRIPGCLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 181
    121 ERISGCLPTIDNGDFSSANKKEYFHGVSYYTCHNLGSGGRKLELVGEPSIYCTSKDDQV 180
OY 182 VGWISGAPACIIPNK 197
    181 VGWISGAPACIIPNK 196
DB 181 VGWISGAPACIIPNK 196

RESULT 9
ID 029528 PRELIMINARY: PRT: 1911 AA.
AC 029528:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE COMPLEMENT RECEPTOR 1 (FRAGMENT).
GN Cr1.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemencia L., Subramanian B.V., Nickells M.W., Hourcade D.E.,
RA Atkinson J.P.,
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U39791; AAA62170.1; -.
DR HSSP: P08603; IHCC.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000834; -.
DR INTERPRO: IPR001424; -.
DR PFAM: PF00084; sushi; 29.
DR PROSITE: PS00087; SOD_CU_2N_1; UNKNOWN_1.
DR PROSITE: PS00133; CARBOXYPEPT_2N_2; UNKNOWN_4.
FT NON_TER 1911
SQ SEQUENCE 1911 AA; 210173 MW; 535A4DD0EAF521D CRC64;

Query Match 70.7%; Score 780; DB 6; Length 1911;
Best Local Similarity 72.3%; Pred. No. 1.1e-72;
Matches 141; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

OY 3 CNAPEWLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 62
    1 CNAPEWLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 62
DB 830 CNAPEWLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 899
OY 63 SCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 122
    1 SCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 122
DB 890 SCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 949
OY 123 RIPCGLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 182
    1 RIPCGLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 182
DB 950 RIPCGLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 1009
OY 183 GWSGAPACIIPNK 197
    183 GWSGAPACIIPNK 197
DB 1010 GWSGAPACIIPNK 1024

RESULT 10
ID 064735 PRELIMINARY: PRT: 483 AA.

```

```

AC 064735;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE COMPLEMENT RECEPTOR RELATED PROTEIN.
GN CrRY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C.
RX MEDLINE=90171600; PubMed=2307848;
RA Paul M.S., Aegeerter-Shaw M., Cepek K., Miller M.D., Wels J.H.;
RT "The murine complement receptor gene family. II. The genomic and
RT transcriptional complexity of the CrRY and CrYps genes.";
RL J. Immunol. 144:1988-1996(1990).
DR EMBL: M34173; AAA37468.1; -.
DR EMBL: M34164; AAA37468.1; JOINED.
DR EMBL: M34165; AAA37468.1; JOINED.
DR EMBL: M34166; AAA37468.1; JOINED.
DR EMBL: M34167; AAA37468.1; JOINED.
DR EMBL: M34168; AAA37468.1; JOINED.
DR EMBL: M34169; AAA37468.1; JOINED.
DR EMBL: M34170; AAA37468.1; JOINED.
DR EMBL: M34171; AAA37468.1; JOINED.
DR EMBL: M34172; AAA37468.1; JOINED.
DR EMBL: M34173; AAA37467.1; -.
DR EMBL: M34164; AAA37467.1; JOINED.
DR EMBL: M34170; AAA37467.1; JOINED.
DR EMBL: M34171; AAA37467.1; JOINED.
DR EMBL: M34172; AAA37467.1; JOINED.
DR EMBL: M34165; AAA37467.1; JOINED.
DR EMBL: M34166; AAA37467.1; JOINED.
DR EMBL: M34167; AAA37467.1; JOINED.
DR EMBL: M34168; AAA37467.1; JOINED.
DR EMBL: M34169; AAA37467.1; JOINED.
DR EMBL: M34170; AAA37467.1; JOINED.
DR HSSP: P08603; IHFI.
DR MGD: MGI:88513; CrRY.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR001005; -.
DR PFAM: PF00084; sushi; 5.
DR PROSITE: PS00037; MYB_1; MISSING (IN LIVER ISOFORM).
FT VARIANT 41 83
SQ SEQUENCE 483 AA; 53762 MW; 259BFED4CE547C1 CRC64;

Query Match 63.6%; Score 702; DB 11; Length 483;
Best Local Similarity 63.6%; Pred. No. 3e-65;
Matches 124; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

OY 3 CNAPEWLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 62
    1 CNAPEWLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 62
DB 85 CNAPEWLPAPRTNLTDEEFPFGTGLNVECRPGYSGRPFSTICLNKSVTGAKDCRR 144
OY 63 SCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 122
    1 SCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 122
DB 145 SCRNPPDPVNGVAVHVIKIQFGSQIKYSGTGRYRLIGSSSACCIISGDTYIMDNETPIC 204
OY 123 RIPCGLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 182
    1 RIPCGLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 182
DB 205 RIPCGLPTIANGDFTSISREYFHGVSYYTCHNLGSRGKVELVGEPSIYCTSKDDQV 264
OY 183 GWSGAPACIIPNK 197
    183 GWSGAPACIIPNK 197
DB 265 GWSGAPACIIPNK 279

RESULT 11
ID 063612 PRELIMINARY: PRT: 497 AA.
AC 063612;

```

DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE 512 ANTIGEN PRECURSOR  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=94161746; PubMed=8117286;  
 RA Sakurada C., Seno H., Dohi N., Takizawa H., Nonaka M., Okada N.,  
 RT "Molecular cloning of the rat complement regulatory protein, 512  
 antigen."  
 RL Biochem. Biophys. Res. Commun. 198;819-826(1994).  
 DR EMBL: D42114; BAA07698.1; -.  
 DR HSSP: P10998; 1VVD.  
 DR INTERPRO: IPR000436; -.  
 DR PFAM: PF00084; sushi; 6.  
 KW Signal.  
 FT SIGNAL 1 36 POTENTIAL.  
 FT CHAIN 37 497 512 ANTIGEN.  
 SQ SEQUENCE 497 AA; 54786 MW; 177AC1IE0FIADIC CRC64;

Query Match 62.4%; Score 689; DB 11; Length 497;  
 Best Local Similarity 64.3%; Pred. No. 7.2e-64;  
 Matches 126; Conservative 17; Mismatches 53; Indels 0; Gaps 0;

QY 2 QCNAPWLPFAPRTNLTDEFEPIGTLYNTECRPGYSGRPSIICLKNSVWTGAKRCRR 61  
 ID 063135 PRELIMINARY; PRT; 559 AA.  
 AC Q63135;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE COMPLEMENT REGULATOR PROTEIN.  
 GN CRRY.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=96006570; PubMed=7590969;  
 RA Ouyg R.J., Lo C.F., Alexander J.J., Sneed A.E., Moxley G. III;  
 RT "Molecular characterization of rat Crry: widespread distribution of  
 RT two alternative forms of Crry mRNA."  
 RL Immunogenetics 42:362-367(1995).  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Dohi N., Sakurada C., Nonaka M., Okada N., Okada H.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U6532; AAA91821.1; -.  
 DR EMBL: D42115; BAA22548.1; -.  
 DR HSSP: P10998; 1VVD.  
 DR INTERPRO: IPR000436; -.  
 DR PFAM: PF00084; sushi; 7.  
 SQ SEQUENCE 559 AA; 61680 MW; 29FL0F6A21DB9B6E CRC64;

Query Match 62.4%; Score 689; DB 11; Length 559;  
 Best Local Similarity 64.3%; Pred. No. 8.3e-64;  
 Matches 126; Conservative 17; Mismatches 53; Indels 0; Gaps 0;

QY 2 QCNAPWLPFAPRTNLTDEFEPIGTLYNTECRPGYSGRPSIICLKNSVWTGAKRCRR 61  
 ID 063135 PRELIMINARY; PRT; 162 AA.  
 AC Q63135;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE COMPLEMENT RECEPTOR 1 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN SEQUENCE FROM N.A.  
 RC MEDLINE=90110163; PubMed=2295627;  
 RA Hourcade D., Mesner D.R., Bee C., Zeldes W., Atkinson J.P.;  
 RT "Duplication and divergence of the amino-terminal coding region of the  
 RT complement receptor 1 (CR1) gene. An example of concerted (horizontal)  
 RT evolution within a gene."  
 RL J. Biol. Chem. 265:974-980(1990).  
 DR EMBL: M31241; AAD15289.1; JOINED.  
 DR EMBL: M31238; AAD15289.1; JOINED.  
 DR EMBL: M31239; AAD15289.1; JOINED.  
 DR EMBL: M31240; AAD15289.1; JOINED.  
 DR HSSP: P02749; 10UB.  
 DR INTERPRO: IPR000436; -.  
 DR PFAM: PF00084; sushi; 2.  
 KW Receptor.  
 FT NON\_TER 162  
 SQ SEQUENCE 162 AA; 17525 MW; B9362CAF8F8ED47 CRC64;

Query Match 61.7%; Score 681; DB 4; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-63;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QCNAPWLPFAPRTNLTDEFEPIGTLYNTECRPGYSGRPSIICLKNSVWTGAKRCRR 61  
 ID 063135 PRELIMINARY; PRT; 162 AA.  
 AC Q63135;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE COMPLEMENT RECEPTOR 1 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN SEQUENCE FROM N.A.  
 RC MEDLINE=90110163; PubMed=2295627;  
 RA Hourcade D., Mesner D.R., Bee C., Zeldes W., Atkinson J.P.;  
 RT "Duplication and divergence of the amino-terminal coding region of the  
 RT complement receptor 1 (CR1) gene. An example of concerted (horizontal)  
 RT evolution within a gene."  
 RL J. Biol. Chem. 265:974-980(1990).  
 DR EMBL: M31241; AAD15289.1; JOINED.  
 DR EMBL: M31238; AAD15289.1; JOINED.  
 DR EMBL: M31239; AAD15289.1; JOINED.  
 DR EMBL: M31240; AAD15289.1; JOINED.  
 DR HSSP: P02749; 10UB.  
 DR INTERPRO: IPR000436; -.  
 DR PFAM: PF00084; sushi; 2.  
 KW Receptor.  
 FT NON\_TER 162  
 SQ SEQUENCE 162 AA; 17525 MW; B9362CAF8F8ED47 CRC64;

OY 122 D 122  
DB 162 D 162

## RESULT 14

ID 099254 PRELIMINARY; PRT: 679 AA.

AC 099254;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE COMPLEMENT RECEPTOR TYPE 2 (CR2) (FRAGMENT).

GN CR2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RX MEDLINE=90229754; PubMed=2139460;

RA Kurtz C.B., O'Toole E., Christensen S.M., Weis J.H.;

RT "The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1."

RL J. Immunol. 144:3581-3591(1990).

RN [2]

RP SEQUENCE OF 21-367 FROM N.A.

RX MEDLINE=95105691; PubMed=7528766;

RA Kim Y.O., Kinoshita T., Molina H., Hourcade D., Seya T., Wagner L.M.,

RA Holers V.M.;

RT "Mouse complement regulatory protein Cr1/p65 uses the specific mechanisms of both human decay-accelerating factor and membrane cofactor protein."

RL J. Exp. Med. 181:151-159(1995).

DR EMBL: U17128; AAA78271.1; -.

DR EMBL: U17123; AAA78271.1; JOINED.

DR EMBL: U17124; AAA78271.1; JOINED.

DR EMBL: U17125; AAA78271.1; JOINED.

DR EMBL: U17126; AAA78271.1; JOINED.

DR EMBL: U17127; AAA78271.1; JOINED.

DR EMBL: M36470; AAA37449.1; -.

DR HSSP: P10998; 1YVD.

DR MGD: MGI:88489; Cr2.

DR INTERPRO: IPR000436; -.

DR INTERPRO: IPR002396; -.

DR PFAM: PF00084; sush1. 10.

DR PRINTS: PR00343; SELECTIN.

FT NON\_TER 679

SQ SEQUENCE 679 AA; 74916 MW; 52FC0DFCED20CDC CRC64;

Query Match 56.5%; Score 624; DB 11; Length 679;

Best Local Similarity 56.8%; Pred. No. 6.7e-57;

Matches 109; Conservative 32; Mismatches 51; Indels 0; Gaps 0;

OY 2 QCNAPFEMLPFARPTNLDEFEPIGYLYNECRPGYSGRPFSTICLKNSVWGAKDCRR 61  
DB 21 QCKLLPKYSFAKSIYSDKSEFAIGTWKCRPGFRKSFITTCLETSTKMSDAQOCRR 80  
OY 62 KSCRNPPDPVNGAVHYIKGIQFSGQIKYSCTKGKRLIGSSSACIIISGDTVIMDNFTIC 121  
DB 81 KPCMNQEPPLHGSVHINTGIEFSTIYSCNQGKRLIGSSSACIIISGDTVIMDNFTIC 140  
OY 122 DRTPCLPRTIANGDFTSISREYFHGVSVTYICNLSRGKKVFEYLGESITCTSKDQ 181  
DB 141 ESIPCESSPFAISNGDFYSSSRDSFFGMYVTYYCHGKNREKLFDLVGEKSIYCTSKDQ 200  
OY 182 VGIMSGPAPOCI 193  
DB 201 VGIMNSPPOCI 212

## RESULT 15

ID 062479 PRELIMINARY; PRT: 330 AA.

AC 062479;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE X/Y PROTEIN (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87196375; PubMed=2952719;

RA Aegerter-Shaw M., Cole J.L., Klickstein L.B., Wong W.W., Fearon D.T.,

RA Lailey P.A., Weis J.H.;

RT "Expansion of the complement receptor gene family. Identification in the mouse of two new genes related to the CR1 and CR2 gene family."

RL J. Immunol. 138:3488-3494(1987).

DR EMBL: M16179; AAA40574.1; -.

DR HSSP: P10998; 1YVD.

DR INTERPRO: IPR000436; -.

DR INTERPRO: IPR001005; -.

DR PFAM: PF00084; sush1. 4.

DR PROSITE: PS00037; MYB.1; UNKNOWN\_1.

FT NON\_TER 1

FT NON\_TER 330

SQ SEQUENCE 330 AA; 36568 MW; FE2A26A15F43B6F2 CRC64;

Query Match 42.9%; Score 474; DB 11; Length 330;

Best Local Similarity 62.0%; Pred. No. 1.4e-41;

Matches 85; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

OY 9 LPFARPTNLDEFEPIGYLYNECRPGYSGRPFSTICLKNSVWGAKDCRRKSCRNPP 68  
DB 194 LPFAKPTNLDESMFPIGYLYECLPGYIKRQFSTICKQDSITWTSABEDCKRCKCKTS 253  
OY 69 DPNVNGAVHYIKGIQFSGQIKYSCTKGKRLIGSSSACIIISGDTVIMDNFTICRPGCL 128  
DB 254 DPENGLVHVTGIEFSGSRINYNQGYRLIGSSSACVITDSDVDTEAPICWIPCEI 313  
OY 129 PRTIANGDFTSISREYF 145  
DB 314 PRCIPNGDFSSSTREDF 330

Search completed: January 13, 2001, 13:49:06  
Job time: 390 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 12:26:35 ; Search time 1005.48 seconds  
(without alignments)  
4118.854 Million cell updates/sec

Title: US-09-380-682-2  
Perfect score: 591  
Sequence: 1 ATGCAGTGCACGCTCCGGA.....AGTCATCATCCGACAA 591

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
31: gb\_est31:\*  
32: gb\_est32:\*  
33: gb\_est33:\*  
34: gb\_est34:\*  
35: gb\_est35:\*  
36: gb\_est36:\*  
37: gb\_est37:\*  
38: gb\_est38:\*  
39: gb\_est39:\*  
40: gb\_est40:\*  
41: em\_estba:\*  
42: em\_estfun:\*  
43: em\_esthum1:\*

44: em\_esthum2:\*  
45: em\_esthum3:\*  
46: em\_esthum4:\*  
47: em\_esthum5:\*  
48: em\_esthum6:\*  
49: em\_esthum7:\*  
50: em\_esthum8:\*  
51: em\_esthum9:\*  
52: em\_esthum10:\*  
53: em\_esthum11:\*  
54: em\_esthum12:\*  
55: em\_esthum13:\*  
56: em\_esthum14:\*  
57: em\_esthum15:\*  
58: em\_esthum16:\*  
59: em\_esthum17:\*  
60: em\_esthum18:\*  
61: em\_esthum19:\*  
62: em\_esthum20:\*  
63: em\_estin1:\*  
64: em\_estin2:\*  
65: em\_estin3:\*  
66: em\_estin4:\*  
67: em\_estov1:\*  
68: em\_estov2:\*  
69: em\_estp11:\*  
70: em\_estp12:\*  
71: em\_estp13:\*  
72: em\_estp14:\*  
73: em\_estp15:\*  
74: em\_estro1:\*  
75: em\_estro2:\*  
76: em\_estro3:\*  
77: em\_estro4:\*  
78: em\_estro5:\*  
79: em\_estro6:\*  
80: em\_estro7:\*  
81: em\_estro8:\*  
82: em\_estro9:\*  
83: em\_estro10:\*  
84: em\_estro11:\*  
85: em\_estro12:\*  
86: em\_estro13:\*  
87: gb\_est41:\*  
88: gb\_est42:\*  
89: gb\_est43:\*  
90: gb\_est44:\*  
91: gb\_est45:\*  
92: gb\_est46:\*  
93: gb\_est47:\*  
94: gb\_est48:\*  
95: gb\_est49:\*  
96: gb\_est50:\*  
97: gb\_est51:\*  
98: gb\_est52:\*  
99: gb\_est53:\*  
100: gb\_est54:\*  
101: gb\_est55:\*  
102: gb\_est56:\*  
103: gb\_est57:\*  
104: gb\_est58:\*  
105: gb\_est59:\*  
106: gb\_est60:\*  
107: gb\_est61:\*  
108: gb\_est62:\*  
109: gb\_est63:\*  
110: gb\_est64:\*  
111: gb\_est65:\*  
112: em\_esthum21:\*  
113: em\_esthum22:\*  
114: em\_esthum23:\*  
115: em\_estom1:\*  
116: em\_estom2:\*

117: em\_estp16:\*

118: em\_estp17:\*

119: em\_estp18:\*

120: em\_estp14:\*

121: em\_estp15:\*

122: em\_estp16:\*

123: em\_estp17:\*

124: em\_estp18:\*

125: em\_estp19:\*

126: em\_estp19:\*

127: em\_estp19:\*

128: em\_estp19:\*

129: em\_estp19:\*

130: em\_estp19:\*

131: em\_estp19:\*

132: em\_estp19:\*

133: em\_estp19:\*

134: em\_estp19:\*

135: em\_estp19:\*

136: em\_estp19:\*

137: em\_estp19:\*

138: em\_estp19:\*

139: em\_estp19:\*

140: em\_estp19:\*

141: em\_estp19:\*

142: em\_estp19:\*

143: em\_estp19:\*

144: em\_estp19:\*

145: em\_estp19:\*

146: em\_estp19:\*

147: em\_estp19:\*

148: em\_estp19:\*

149: em\_estp19:\*

150: em\_estp19:\*

151: em\_estp19:\*

152: em\_estp19:\*

153: em\_estp19:\*

154: em\_estp19:\*

155: em\_estp19:\*

156: em\_estp19:\*

157: em\_estp19:\*

158: em\_estp19:\*

159: em\_estp19:\*

160: em\_estp19:\*

161: em\_estp19:\*

162: em\_estp19:\*

163: em\_estp19:\*

164: em\_estp19:\*

165: em\_estp19:\*

166: em\_estp19:\*

167: em\_estp19:\*

168: em\_estp19:\*

169: em\_estp19:\*

170: em\_estp19:\*

171: em\_estp19:\*

172: em\_estp19:\*

173: em\_estp19:\*

174: em\_estp19:\*

175: em\_estp19:\*

176: em\_estp19:\*

177: em\_estp19:\*

178: em\_estp19:\*

179: em\_estp19:\*

180: em\_estp19:\*

181: em\_estp19:\*

182: em\_estp19:\*

183: em\_estp19:\*

184: em\_estp19:\*

185: em\_estp19:\*

186: em\_estp19:\*

187: em\_estp19:\*

188: em\_estp19:\*

189: em\_estp19:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	279.4	47.3	444	24	A1718588	A1718588 as46h01.x
C 2	267.4	45.2	465	109	BE552138	BE552138 hw29d02.x
C 3	263.2	44.5	650	93	AM610808	AM610808 up37f12.x
C 4	259.4	43.9	443	17	A1240881	A1240881 qj94e04.x
C 5	248	42.0	611	96	AM851015	AM851015 IL3-CT02
C 6	235.6	39.9	549	96	AM919879	AM919879 EST351183
C 7	215.2	36.4	356	24	A1735459	A1735459 att1h03.x
C 8	211.8	35.8	981	137	BE917021	BE917021 601663678
C 9	211.2	35.7	488	139	BF023537	BF023537 ux09c08.y
10	210	35.5	525	4	AA286570	AA286570 vb76a03.x
11	204	34.5	441	95	AM825298	AM825298 us13d06.y
12	203	34.3	614	2	AA107525	AA107525 mp08b07.r
13	197.6	33.4	601	3	AA212152	AA212152 mb80g07.r
14	191.4	32.4	684	3	AA186185	AA186185 mc63d04.x
15	187.6	31.7	654	17	A1194601	A1194601 ue69b04.r
16	174.4	29.5	389	145	T66823	T66823 ya50d08.s3
C 17	170.8	28.9	433	24	A1735085	A1735085 as44f09.x
C 18	168	28.4	643	96	AM912091	AM912091 u41f04.y
19	159.2	26.9	327	158	AO529858	AO529858 RPT-11-3
20	155.8	26.4	409	38	AM012541	AM012541 u006c01.y
21	155.8	26.4	409	38	AM012541	AM012541 u006c01.y
22	154.4	26.1	643	3	AA153888	AA153888 mq56d05.r
23	152	25.7	320	151	AQ266148	AQ266148 C1EB1-E1-
24	146.2	24.7	541	146	T83269	T83269 yd41a11.r1
25	144.4	24.0	387	87	AM211552	AM211552 uc82e02.y
26	142	24.0	346	145	T66824	T66824 ya50b08.r3
27	141.8	24.0	327	141	H31617	H31617 EST105833 R
28	140.2	23.7	469	4	AA261275	AA261275 vD03b10.r
29	135.2	22.9	613	106	BE308463	BE308463 601090308
30	134.8	22.8	544	4	AA271926	AA271926 vb75c04.r
31	129.4	21.9	355	145	T27695	T27695 EST12512 Hu
32	126.8	21.5	382	13	AA683947	AA683947 vx87b09.r
33	123.8	20.9	431	139	BF015454	BF015454 uy21g02.y
34	115	19.5	419	11	AA174888	AA174888 ms77g05.r
35	112.8	19.1	835	3	AA174888	AA174888 ms77g05.r
36	111.4	18.8	550	91	AM519788	AM519788 up39d05.y
37	109	18.4	550	91	AM502222	AM502222 ut-HF-BR0
38	105	17.8	440	142	H73873	H73873 ys14d08.r1
39	103	17.4	499	13	AA895111	AA895111 yv07b12.r
40	85.2	14.4	527	158	AQ492897	AQ492897 HS_5126.A
41	85	14.4	356	14	AA982230	AA982230 ua49b04.r
42	81	13.7	660	2	AA145452	AA145452 mr79g11.r
43	76	12.9	564	13	AA895456	AA895456 vx65a07.r
44	75	12.7	370	111	BE655649	BE655649 ut-M-BH0
45	73.6	12.5	388	10	AA655637	AA655637 vs43a01.r

## ALIGNMENTS

RESULT 1  
A1718588/c  
LOCUS  
DEFINITION  
IMAGE:2320273.3' similar to gb:Y00816\_cds1 COMPLEMENT RECEPTOR TYPE  
1. PRECURSOR (HUMAN), mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
A1718588 444 bp mRNA  
A1718588  
A1718588.1 GI:5035844  
EST  
10-JUN-1999



RESULT	2
LOCUS	BE552138/c
DEFINITION	BE552138 465 bp mRNA
ACCESSION	hw29602.x1 NCI_CGAP_kid1 Homo sapiens cdna clone IMAGE:3184323
VERSION	(HUMAN), mRNA sequence.
KEYWORDS	EST.
SOURCE	BE552138.1 GI:9793830
ORGANISM	human.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 465)
JOURNAL	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997) Tumor Gene Index Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher Koskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: inf@image.llnl.gov Seq primer: -40UP from Glibco High quality sequence stop: 456. Location/Qualifiers 1..465 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="3184323" /clone_lib="NCI_CGAP_Kid1" /lab_host="DH10B" /note="Organ: Kidney; Vector: pUT3D-Pac (Pharmacia) with a modified polylinker, site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAV purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from a pool of 5,000 clones made from the same library (clones 1323376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo." Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	134 a 85 c 107 g 139 t
ORIGIN	
Query Match	45.2% Score 267.4; DB 109; Length 465;
Best Local Similarity	83.3%; Pred. No. 3.6e-75;
Matches 304; Conservative	0; Mismatches 61; Indels 0; Gaps 0;
4 CAGTGCAACGCTCCGGAATGGCTGCCTTCGCCGCCGACCACACTGACTGTAATT	63
DB 450 CAATGCATGTCCCGAATGGCTTCATTTGGCAGCGCTACCAACCTACTGATCTT	391
64 GAGTCCCGAGGACTACCTGAACTGAACTACGAAATCCCGGGTTATAAGCGCCGCCG	123
DB 390 GAGTTTCCCATTTGGGACAATATCTGAACTAATAATGCCCCCTGGTTATTCGGAAGACCG	331
QY 124 TTTTCTATCATCTGCTGTAATAAACCTCTCTGCACTGTGCTTAAGACCGTTGCGGAGGT	183
DB 330 TTTTCTATCATCTGCTGTAATAAACCTCTCTGCACTGTGCTTAAGACCGTTGCGGAGGT	271
QY 184 AATCTGTCTATCCGCCGATCCGGTTAAGCGCATGTGATGATCAAAAGGCAT	243

Oy	244	CAGTTCGGTCCCAATTAATATCTTGTTACTAAAGGTACCGCTGATTGCCTCC	303
Dd	210		151
Oy	304	AGCGCTACATCATCTCTGGTGCATCTCATTTGGATTAATGAACAACCGATTGT	363
Dd	150		91
Oy	364	GACCGC 368	
Dd	90	GACAG 86	
RESULT	3		
LOCUS	AM610808		
DEFINITION	AM610808 650 bp mRNA EST 23-MAR-2000 up37f12.x1 Soares_mouse_MNGB_bcell Mus musculus cDNA clone IMAGE:2699183 3' similar to gb:M3529 Mus musculus complement receptor (MOUSE);, mRNA sequence.		
ACCESSION	AM610808		
VERSION	AM610808.1		
KEYWORDS	GI:715549		
SOURCE	EST.		
ORGANISM	house mouse. Mus musculus.		
REFERENCE	Mammalia; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 650) NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.		
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
TITLE	Unpublished (1997)		
JOURNAL	Other_ESTS: up37f12.y1		
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1034707		
FEATURES	High quality sequence stop: 453.		
source	Location/Qualifiers 1..650 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:2699183" /clone_1lb="Soares_mouse_MNGB_bcell" /lab_host="DH10B (phage-resistant)" /note="Organ: germinal B-cell; Vector: pUT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TCTTACCATCTGGAAGTGGAGCGGCCCGCTGTTTTTTTTTTTTTTTTTTTTTTT T3'):: double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT73 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."		
BASE COUNT	174 a 154 c 182 t		
ORIGIN			
Query Match	44.5%; Score 263.2; DB 93; Length 650;		
Best Local Similarity	65.5%; Pred. No. 8.7e-74;		
Matches 385; Conservative	0; Mismatches 203; Indels 0; Gaps 0;		
Oy	4	CAGTGCACAGCTCCGGAATGCTGCCGTTGGCGGCGCCGACCAACCTGACTGATGATTT	63
Dd	54		113
Oy	64	CAGTTCGGATCGGTACTCTGACTGATACGATGCCGCGGGGTATACGGCCGCCG	123
Dd	173		173

QY	124	TTTTCTCATCATCGCCGCGAAACATCGTGTGGACGTGCTTAAGACCGCTTGCCACGCT	183
Db	174	TTCTCTATACACCTTCCCAACAAGACTCAACTGCACAGCTCTCAAGATAGTATATACGA	233
QY	184	AAATCTTGCTGTAATCCGCAGATCCGGTTAACGGCATGCTGATGATCAAAAGCATC	243
Db	234	AAACAATGATAAATCTCTTGAGATCCCGAAGATGGCTTGATACATGACACAGGCAT	293
QY	244	CAGTTGCTGCCCAATTAATATCTTGTAAGTAAAGTTAACGTCGATGGTGGTCTCC	303
Db	294	CAGTTGGATCCCGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	353
QY	304	AGCCCTACATGACATCATCTCGTGTGATACTGTCAATTTGGATAATGAACACCGATT	363
Db	354	TTCTGTGATGATGTCACACACTGATCAAAAGTGTGATGGATGACTGAGCAGCAT	413
QY	364	GACCGAATTCGGTGTGCTGTCGCCGCCACCATCGCCCAAGGTATTTACCTCATAC	423
Db	414	GAGTGATATCTTGATGAGATACCCCGACGATTCACATGAAGATGATTTCTTCA	473
QY	424	CGCGATTTTTCATGATGTTCTGTGTGATCATACCATGTCATCTGGGTAGCCGT	483
Db	474	AGAGAAGACTTTCATTAATGAATGTGTTTACCTACCGCTGCAACATGATGGAG	533
QY	484	AAAAAGTGTGTGAGCTGCTGGGTGAGCCGTGCATCTACTGACATGACCAAGAT	543
Db	534	AAGGGCTCTTTAACTGCTGCTGGGTGAGCCCTCTTAACTGATACACACGAT	593
QY	544	GTGGCATCTGAGAGCGCGCCGCGACCGGACGATGATATCCGACAA	591
Db	594	ATTGAGTCTGGAGCGGACCTCTCTGATGATTAATCACTCAACAG	641
RESULT	4		
LOCUS	AI240881/c		
DEFINITION	AI240881	443 bp	mRNA
ACCESSION	qj44e04.x1	NCI-CGAP_K1d3	EST
VERSION	similar to gp.i00816.cdsl	COMPLEMENT	RECEPTOR TYPE 1 PRECURSOR
KEYWORDS	(HUMAN); mRNA sequence.		
SOURCE	AI240881		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
JOURNAL	1 (bases 1 to 443)		
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.		
	Emmert-Buck, M.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/MLN at:		
	www.bio.lnlnl.gov/brp/image/image.html		
	Insert length: 625	Std Error: 0.00	
	Seq primer: -40up from Gibco		
	High quality sequence stop: 373.		
FEATURES	Location/Qualifiers		
source	1..443		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1867134"		
	/clone_lib="NCI-CGAP_K1d3"		
	/lab_host="DH10B"		
	/note="Organ: kidney; Vector: PT773D-Pac (Pharmacia) with		

a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonalido.

BASE COUNT 131 a 80 c 104 g 128 t  
ORIGIN

Query Match 43.9%; Score 259.4; DB 17; Length 443;  
Best Local Similarity 81.9%; Pred. No. 1.3e-72;  
Matches 299; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 4 CAGTGCACCGCTCCGGAATGCTGCGTCCGCCGCCGACCACTGACTGATGAAATT 63  
DB 442 CAATGCAATGCGGGAATGGGCTTCATTTGCCAGGCTACCACTGATGATGATCT 383  
QY 64 GAGTCCCGATCGTACCTGACCTGATGATGATGATGATGATGATGATGATGATG 123  
DB 382 GAGTTCCCATGGGACATCTGACTGATGATGATGATGATGATGATGATGATGATG 323  
QY 124 TTTTCTATCATCTGCGTGAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183  
DB 322 TTTTCTATCATCTGCGTGAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263  
QY 184 AAATCTGCTGATCCGCGGATCCGCTGATGATGATGATGATGATGATGATGATGATG 243  
DB 262 AAATCATGTGTATCTCTCCGATCTCTGATGATGATGATGATGATGATGATGATG 203  
QY 244 CAGTGGTCCCAATTAATATCTGATGATGATGATGATGATGATGATGATGATGATG 303  
DB 202 CAGTGGTCCCAATTAATATCTGATGATGATGATGATGATGATGATGATGATGATG 143  
QY 304 AGGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363  
DB 142 TCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 83  
QY 364 GACCG 368  
DB 82 GACAG 78

RESULT 5  
AM851015/c 611 bp mRNA EST 19-MAY-2000  
LOCUS IL3-CT0220-150200-069-607 CT0220 Homo sapiens cDNA, mRNA sequence.  
DEFINITION AM851015  
ACCESSION AM851015.1 GI:7946532  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 611)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordoli,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,U.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 2002663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922

Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=62-IL3-CT0220-150200-069-607/ct3-2000-02-15&rl=1)  
Seq primer: puc 18 forward  
High quality sequence start: 7  
High quality sequence stop: 544.  
Location/Qualifiers  
1. 611  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0220"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site: 1; Smal; Site: 2; Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 143 a 153 c 155 g 160 t  
ORIGIN

Query Match 42.0%; Score 248; DB 96; Length 611;  
Best Local Similarity 77.9%; Pred. No. 6.7e-69;  
Matches 299; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 208 CCGGTACGGCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 267  
DB 611 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 552  
QY 268 TCTGTACTAAGGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATG 327  
DB 551 TCTGTACTAAGGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATG 422  
QY 328 GATACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 387  
DB 491 AATACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432  
QY 388 CCGACCATGCGCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 447  
DB 431 CCAACCATGCGCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 372  
QY 448 GTGTGACTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507  
DB 371 GTGTGACTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312  
QY 508 GAGCGCTCATCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 567  
DB 311 GAGCGCTCATCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 252  
QY 568 CCGCATGCTATCTCCGCAACAA 591  
DB 251 CCTCAGTGCATTTACTTAACAA 228

RESULT 6  
AW919879 549 bp mRNA EST 25-MAY-2000  
LOCUS EST351183 Rat gene index, normalized rat, norvegicus, Bento Soares  
DEFINITION AW919879  
ACCESSION AW919879  
VERSION AW919879.1 GI:8085663  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 549)

**AUTHORS** Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J.,  
 Kerlavage, A.R., and Adams, M.D.  
**TITLE** Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat  
 Gene Index  
**JOURNAL** Unpublished (1998)  
**COMMENT** Contact: Lee, NH  
 ATCC

The Institute for Genomic Research  
 9712, Medical Center Drive, Rockville, MD 20850, USA  
 Tel: (301)-838-3529  
 Fax: (301)-838-0208  
 Email: nhlee@tigr.org  
 This clone is available through the ATCC, contact the ATCC  
 tel#703-365-2700 for further information  
 Seq primer: M13 Reverse.

**FEATURES**  
 source

1..549  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone\_id="RGIN94"  
 /clone\_lib="Rat gene index, normalized rat, norvegicus,  
 Bento Soares"  
 /issue\_type="mix - brain, ovary, placenta, kidney, lung,  
 liver, embryo, heart, muscle, spleen"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Estimated insert size approx.1 kb"  
 BASE COUNT 148 a 127 c 120 g 154 t  
 ORIGIN

Query Match 39.9%; Score 235.6; DB 96; Length 549;  
 Best Local Similarity 66.6%; Pred. No. 6,4e-65;  
 Matches 337; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 86 TGAACACAGATGCGCGGGTATAGCGCGCGCGCTTTCATCATCTGCTGAAA 145  
 Db 5 TGAAGTATGAATGCTTTAGATATATCAAGAGCATCTCTCATACCTCGAAGTAA 64  
 QY 146 ACTCTGTGAGTGTGCTTAAGACCGTTCGCGAGTAATCTGTCTAATCCGCCAG 205  
 Db 65 ATCAGATGAGCAATCTCTCAAGAGCTGTATAGTAAACAAGTGAACCTCTTTC 124  
 QY 206 ATCCGCTTAACGGCATGTGATGATCAAGGCAATCCAGTTCCGTTCCCAATTAA 265  
 Db 125 ATCCCTCAGATGGCATGATGATCAAGGCAATCCGTTCCGTTCCCTATCATT 184  
 QY 266 ATTCTGTACTAAGGTACCGTCTGATGTTCCCTCCAGCGCTACATGATCATCTG 325  
 Db 185 ATACCTGTATGAAGATACCGCTCATGTTCTCTCTCTGATGATGATCATCTG 244  
 QY 326 GTGATACGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 385  
 Db 245 ATCAGATGAGTGTGCTGAGTTCGAGGACCACTATTGTGATCAATCTCTGAGATAC 304  
 QY 386 CGCGGACATCGCCAGACGATGATGATGATGATGATGATGATGATGATGATG 445  
 Db 305 CCCCAGCATTCCTCCATGAGATTTCTCAGTCTTAACAGAGAAATTTTCATTA 364  
 QY 446 CTGTGCTGATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 505  
 Db 365 TGTGATGATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 424  
 QY 506 GTGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 565  
 Db 425 GTGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 484  
 QY 566 CACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
 Db 485 CTCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 510

RESULT 7

AT735459/c  
 LOCUS AT735459 356 bp mRNA EST 14-JUN-1999  
 DEFINITION at11i03.x1 Bartsed aorta HPLRB6 Homo sapiens CDNA clone  
 IMAGE:2354837.3 similar to gb:Y00816.cdsl COMPLEMENT RECEPTOR TYPE  
 1 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AT735459  
 VERSION AT735459.1 GI:50569683  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 356)  
 HILLIER, L., ALLEN, M., BOWLES, L., DUBUQUE, T., GEISEL, G., JOST, S.,  
 KILZMAN, D., KUCABA, T., LACY, M., LE, N., LENNON, G., MARRA, M., MARTIN  
 J., MOORE, B., SCHELLENBERG, K., STEPTOE, M., TAN, F., THEISING, B.,  
 WHITE, Y., WYLLIE, T., WATERSTON, R., and WILSON, R.  
 WashU-NCI human EST Project  
 Unpublished (1997)  
**TITLE** Unpublished (1997)  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -400P from GIBCO.

**FEATURES**  
 source

1..356  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="2354837"  
 /clone\_lib="Bartsed aorta HPLRB6"  
 /sex="male"  
 /dev\_stage="adult, age 64"  
 /lab\_host="DH10B (phage resistant)"  
 /note="Organ: aorta; Vector: p773D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCGATGAGGAGGCGCGCGCGCTTTCTTTCTTTCTTTCTTTCTTTCTTT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 [5' AATCGGATCGAAC 3' and 5' GTGATCGAG 3'], digested  
 with NotI and cloned into the NotI and Eco RI sites of  
 the modified p773 vector. Library constructed by Bob  
 Bartsed."

BASE COUNT 107 a 61 c 77 g 111 t  
 ORIGIN

Query Match 36.4%; Score 215.2; DB 24; Length 356;  
 Best Local Similarity 84.9%; Pred. No. 2.1e-58;  
 Matches 241; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 85 CTGACATGAGATGCGCGCGGGTATAGCGCGCGCGCTTTCATCATCTGCTGAAA 144  
 Db 355 CTGACATGAGATGCGCGCGGGTATAGCGCGCGCGCTTTCATCATCTGCTGAAA 296  
 QY 145 AACTCTGTGAGTGTGCTTAAGACCGTTCGCGAGTAAATCTGTGTAATCGCCA 204  
 Db 295 AACTCAGTCTGGACAAGTGTAAAGCAAGTGAAGCAAGTGAATCATGCTTAATCTTCCA 236  
 QY 205 GATCCGGTTAAGCGATGTGATGATGATGATGATGATGATGATGATGATGATG 264  
 Db 233 GATCCTGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 176  
 QY 265 TATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 324  
 Db 175 TATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 116  
 QY 325 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 368  
 Db 115 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 72

```

RESULT      8
BE917021    981 bp      mRNA      EST      29-SEP-2000
LOCUS       6016387881 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3964170 5',
DEFINITION  mRNA sequence.
ACCESSION   BE917021
VERSION      BE917021.1 GI:10418246
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 981)
AUTHORS     NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM9133 row: k column: 19
            High quality sequence stop: 647.
            Location/Qualifiers
                source          1..981
                                /organism="Mus musculus"
                                /strain="FVB/N"
                                /db_xref="taxon:10090"
                                /clone="IMAGE:3964170"
                                /clone_1lb="NCI CGAP Mam1"
                                /tissue_type="tumor, biopsy sample"
                                /dev_stage="3 months, virgin"
                                /lab_host="DH10B"
                                /note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI;
                                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                                library constructed by Life Technologies. Investigator
                                providing samples: Gilbert Smith, NIH"

BASE COUNT   247 a      267 c      232 g      235 t
ORIGIN
Query Match      35.8%; Score 211.8; DB 137; Length 981;
Best Local Similarity 64.8%; Pred. No. 3,4e-57;
Matches 362; Conservative 0; Mismatches 192; Indels 5; Gaps 3;

```

```

Db 321 TCTGCTGATGTGTCATCATCACTCAAAAGTGTGATGGGATACAGCAGCACTATTGT 380
Oy 364 GACCGAATTCGGTGTGCTGCCGCGACCAATGCCAGGATTTCACTATCACT 423
Db 381 GAGTGATTCCTGTGAGATACCCCGAGCAATCCCAATGAGA-TTCTTCAGTTCAACC 439
Oy 424 CCGGATATTTTCATATGTTCTGTGGTACCTACACATGCATTCGATGCGGTGT 483
Db 440 AAGAGAAGACTTCATATGGAATGGTGTACCTACC-GTGCACACATGATCGAGAGG 498
Oy 484 AAAAGGTTGTAGCTGTGGTGGAGCGGTCACATCACTAGCAAGCAAGATCA 543
Db 499 AAGGCCCTTTAACTGTGGGTGGAGGCTCTTAACTGACGACGATGCTGAA 558
Oy 544 GTGGGCACTGAGAGCGGCC 562
Db 559 ATTGGAGTCTGAGCGGCC 577

RESULT      9
BF023537    488 bp      mRNA      EST      10-OCT-2000
LOCUS       ux09c08.y1 Soares_thymus_2ndmt Mus musculus cDNA clone
DEFINITION  IMAGE:3470990.5' similar to TR:Q61447 Q61447 COMPLEMENT RECEPTOR
            RELATED PROTEIN. ; mRNA sequence.
ACCESSION   BF023537
VERSION      BF023537.1 GI:10754870
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 488)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1390350
            Seq primer: -40RP from Glibco
            High quality sequence stop: 439.
            Location/Qualifiers
                source          1..488
                                /organism="Mus musculus"
                                /strain="C57BL/6J"
                                /db_xref="taxon:10090"
                                /clone="IMAGE:3470990"
                                /clone_1lb="Soares_thymus_2ndmt"
                                /sex="male"
                                /tissue_type="thymus"
                                /dev_stage="4 weeks"
                                /lab_host="DH10B"
                                /note="Vector: p773D-Pac (pharmacia) with a modified
                                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                                was primed with a Not I - oligo(dT) primer [5';
                                TGTTCACATCTGAGAGTGAGAGCGCCGCTTTTCTTTTCTTTTCTTTT
                                3']; double-stranded cDNA was ligated to Eco RI adaptors
                                (pharmacia), digested with Not I and cloned into the Not I
                                and Eco RI sites of the modified p773 vector. RNA
                                provided by Dr. Bertrand Jordan. Library went through two
                                rounds of normalization, and was constructed by Bento
                                Soares and M.Fatima Bonaldo."

BASE COUNT   135 a      113 c      100 g      140 t
ORIGIN
Query Match      35.7%; Score 211.2; DB 139; Length 488;
Best Local Similarity 65.9%; Pred. No. 4,4e-57;

```

		/clone="IMAGE:762892"	
		/clone_lib="Soares mouse 3MNE12 5"	
		/sex="unknown"	
		/issue_type="fetus"	
		/dev_stage="12.5dpc total fetus"	
		/lab_host="DH10B"	
		/note="Organ: whole fetus; Vector: pT73D-Pac (Pharmacia)	
		with a modified polylinker; Site 1: Not I; Site 2: Eco RI;	
		1st strand cDNA was primed with a Not I - oligo(dT) primer	
		[5', TGTTCCAAATCGAAGTAGGACGGCGGCCCTCATTTTTTTTTTTTTT	
		3'], on total mouse RNA [provided by Minoru Ko, Wayne	
		State Univ.]; double-stranded cDNA was ligated to Eco RI	
		adaptors (Pharmacia), digested with Not I and cloned into	
		the Not I and Eco RI sites of the modified pT73 vector.	
		Library went through one round of normalization, and was	
		constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT	146 a	123 c	111 g 145 t
ORIGIN			
Query Match	Best Local Similarity	35.5%; Score 210; DB 4; Length 525;	
	Matches 312; Conservative	64.7%; Pred. No. 1,le-56;	
		0; Mismatches 170; Indels 0; Gaps 0;	
QY	4 CAGTGCAACGCTCCGGATGSGCTGCCGTGGCGCCGCACAACCTGACTGAATTT	63	
Db	37 CACGCCCCAGCCCACATCACAGCTTCCTTGCCAAACCTATAATCACTGATGAATCC	96	
QY	64 GAGTCCCGATCGGTACCCTCCTGACATGACGAATGCGCGCGGGTTAPGGCGCGCCG	123	
Db	97 ATGTTCCCATGGAACATATTTTGTGTATGAAATGTCTCCAGATATATCAAGAAGCAG	156	
QY	124 TTTTCTATCATCTGCTGAAAACTGTGTCTGACTGAGTGTGTAAGACCGTTGCCGACT	183	
Db	157 TTCTCTACACCTGCAACAAGACTCAACCGGACGAGTGTGAAGTAAAGTGAATACGA	216	
QY	184 AAATCTGTGCTAATCCGCGCATCCGGTTAAGCGCATGGGCGCATGATCAAAAGCATC	243	
Db	217 AAAACAATGTAAACTCCTTCAGATCCTCGAAGATGCTTTGGTACTGTGACACAGSATT	276	
QY	244 CAGTTCGGTCCCAATTAATATCTCTGTGACTAAGATTACCGTCTGATGGTTCCTCC	303	
Db	277 CAGTTTGAGATCCGCTATTAAATTACTTGTAAATCAAGATACCGCCCTCATGGTCTCC	336	
QY	304 AGCGTACATGCATCATCTCTGTGTGATACGTCAATTTGGGATAATGAACACGATTTGT	363	
Db	337 TCCTCTATGTGTCACTGATCAACAAGTGTGATTGGGAACCTGAGCACTAATTTGT	396	
QY	364 GACCGAATTCGCTGTGCTGCGCCGACCATGGCAACGAGTATTACCTCATAGT	423	
Db	397 GAGTGGATTCCTGTGTGAGATACCCCGACGAGATTCCCAATGAGATTTCTTCATGTC AAC	456	
QY	424 CGCAGATATTTTCACTATGTTCTGTGTGTGACCTACCATGCAATCTGGGTAGCCGTGT	483	
Db	457 AGAAGAACCTTCATTATGGAATGTGATTACCTACCGCTGCAACAACCTGATGAGAGGG	516	
QY	484 AA 485		
Db	517 AA 518		
RESULT 11			
LOCUS	AM825298		
DEFINITION	usl3a06.YI Soares NMGB_C-cell Mus musculus CDNA clone		
ACCESSION	AM825298		
VERSION	AM825298.1 GI:7918375		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Fukurovata Metazoa; Chordata; Vertebrata; Mammalia; Muridae; Mus musculus		



RESULT	13
AA212152	
LOCUS	601 bp mRNA
DEFINITION	mus80607.r1 Strataegene mouse melanoma (#937312) EST 31-JAN-1997
	clone IMAGE:651900 5 similar to gb:423529 Mus musculus cDNA
	receptor (MUSE)'; mRNA sequence.
ACCESSION	AA212152
VERSION	AA212152.1 GI:1810867
KEYWORDS	EST.
SOURCE	mouse muscu.
ORGANISM	Mus musculus

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse Est Project Unpublished (1996)		
Contact: Marra M/Mouse Est Project WashU-HHMI Mouse Est Project		
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
Tel: 314 286 1800 Fax: 314 286 1810		
Email: mouseest@watson.wustl.edu		
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:397748		
Seq primer: -28ml3 rev1 ET from Amersham		
High quality sequence stop: 280.		
Location/Qualifiers		
1..601		

```

/lab-host="SOLR (Kanamycin resistant)"
/nodec="Organ: skin; Vector: pBluescript SK-; Site-1: EcoRI
; Site-2: XhoI; Cloned unidirectionally. Primer: 019g
df. From M2 cells, a highly metastatic derivative of the
K-1235 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACACGAC
3', -3' adaptor sequence: 5' CTCGAGTGTGTTTTTTTTTTTTTTT 3"
149 a 137 c 140 g 175 t

```

Query Match	33.48;	Score 197.6;	DB 3;	Length 601;
Best Local Similarity	64.88;	Pred. No. 1.1e-52;		

RESULT	14
AA186185	
LOCUS	
DEFINITION	AA186185 684 bp mRNA
	me63d04.r1 Soares_thymus.2NDMT Mus musculus cDNA clone IMAGE:634567
	5' similar to gb:U00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR
	(HUMAN); gb:M23529 Mus musculus complement receptor (MOUSE);, mRNA
	sequence.
ACCESSION	AA186185
VERSION	AA186185.1
KEYWORDS	GI:1772023
SOURCE	EST.
	house mouse.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (Bases 1 to 684)			
	Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kueba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellendberg, K., Stepcie, M., Tan, F., Underwood, R., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.	The WashU-HMNI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project WashU-HMNI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAG Consortium (info@image.lnl.gov) for further information. MW1:386559
				Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 431.

FEATURES	Location/Qualifiers
source	1..684
	/organism="Mus musculus"
	/strain="C57BL/6J"



```

/db_xref="taxon:10090"
/clone_image="634567"
/clone_lib="Soares_thymus_2nbmt"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7TD-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5].
TGATCCCATCTGAGGTGGAGCGGCCCGTTTATTATTTTATTTTATTTT
3'] double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7D3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fátima Bonaldo."

```

Query Match	32.48;	Score 191.4;	DB 3;	Length 684;
Best Local Similarity	66.08;	Pred. No. 1.1e-50;		
Matches 276; Conservative	0;	Mismatches 142;	Indels 0;	Gaps 0;

QY	174	TTGCCGAGTAAATATCTGGTCGTAATCCGACAGATCCGGTTAAGCGGATGGTGCATGTAT	233
Db	208	TTTCATTAGGAACAACATGTAAAACTCCTCAGATCCTCGAATGGCTTGTTGTAATGTACA	267
QY	234	CAAAAGCATCCAGTTCGGTTCGATTAATTAATTCCTGTAACAAAGGTATACCGTTCGAT	293
Db	268	CACGAGCATTCAGTTTGGATCCCGATTAAATTAATCTTAATCAAGGATACCGCTCAT	327
QY	294	TGGTTCCTCCAGCGCTAACATGCATCATCTCTGGTGTACTGTCAATTTGGGATATGAAC	353
Db	328	TGGTTCCTCCTCTCGCTGTATGTGTCTATCATCTGATCAAAAGTGTGATTTGGGATACTGAGC	387
QY	354	ACCGATTTGTGACCGAATTCGAGTGTGTGCGCGCGGACATCGGCCAAGGAGTATTCAC	413
Db	388	ACCTATTGTGTAGTGATATCTTGTAATACCCCGACGATCTCCAAATGGAAATTTCTT	447
QY	414	CTCTATCATGATCCGAGTATTTTCACATATGTTCTGTGTGAGCTACCATCGCATCTCGG	473
Db	448	CAGTTCAACCAAGAGAAGACTTTCATATATGGAATGGTGGTTACTACCGGTGCACACATGA	507
QY	474	TAGCGGTGTAATAAAGTGTTTTGAAGTCTGTGGTGAAGCCGTTCATTTACTGCATCTAACA	533
Db	508	TTCGAGAGGGAAGGCGCTTTTAACCTGTGGGTGAGCCCTCTTATTAGTGTACCAACA	567
QY	534	AACAGATCAAGTGGGATCTGGAGCGCGCCCGGACCGGACGCGATCATATCCCAACAA	591
Db	568	CGATGTGTGATTTGAGTCTGGAGCGGCGCTCTCTCATGATGATTAACCTCAACA	625

	RESULT	15
LOCUS	AI194601	
DEFINITION	AI194601 654 bp mRNA EST 14-OCT-1998	
ACCESSION	U69B04.1	
VERSION	U69B04.1	
KEYWORDS	similar to gb:Y00816.cdsl COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HDMAN); gb:M23529 Mus musculus complement receptor (MCUSE);, mRNA sequence.	
ORGANISM	house mouse.	
SOURCE	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 654)	
AUTHORS	Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisling, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and	

**TITLE** Materston, R.H.  
**JOURNAL** The WashU-HHMI Mouse EST Project  
**COMMENT** Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watsn.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:333939  
 Trace considered overall poor quality  
 Seq primer: -28m13 rev2 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..654

## FEATURES

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone IMAGE:1496335
/clone_lib="Soares_NMPu"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
Oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Donaldso. "

```

Query Match	31.7%;	Score 187.6;	DB 17;	Length 654;
Best Local Similarity	66.7%;	Pred. No. 1.9e-49;		
Matches 268;	Conservative	0;	Mismatches 134;	Indels 0;
			Gaps	0;

OY	151	GTCTTAAGGACCGTTGGCCGACGTAAACTGTGTGTGTAATCCGACAGTACCGGTTAACGGCA	220
DB	2	GTGCGAAGATAGTAAGTATATCGAAGACAAATGTAATACTCTTAGATGCTGAGAAAGGCT	61
OY	221	TGCTGCATGTGATCAAGGCAATCCAGTTCGGTTCGCCAATAATTAATTTCTTGTACTAAAG	280
DB	62	TGTATACATGTACACACAGAGCACTTAGTTGGATCCGATTAATTTACTTGTGATCAAG	121
OY	281	GTTACCGCTGTGATTTGGTTCCCTCCAGCGCTACATGATCATCTCTGTGTACTGTATCTT	340
DB	122	GATACCGGCTATGTTGTTCCCTCCCTCTGCTATATGTGTCGCACTGATCAAAAGTGTGATT	181
OY	341	GGGATTAATGAAACACGATTTTGTGACCGAATCCGTGTGTGTGTCGCGCCGACATGCCA	400
DB	182	GGGATGCTGAGGACACCTATTTGTGTAGTGATTCCTTGTGATTAACCCACAGGATTCCTA	241
OY	401	ACGGATATTACCTCTATCATAGTGCAGATTTTTCACATAGTGTCTGTGTGATCCATCC	460
DB	242	ATGGAGATTTTTCATAGTTCCAAACCGAATAAGTTTCAATTATGSAATGGTGTACTAC	301
OY	461	ACTGCATCTGGGTAGCCCGTGTGTAAAGGTGTTTGAAGCTGTGGGTGAACCGTCCATCT	520
DB	302	GCTGCACACACTGATGCGAGAGGAGGAGCGCTTTTAACTCGTGGGTGAGCCCTCTTAT	361
OY	521	ACTGCACATGAAAGAGATCAATGTGGCATCTGGAGCGCC	582
DB	362	ACTGTACCGACAGATGTGTAAATTTTGGATCTGGAGCGGCC	403

Search completed: January 13, 2001, 12:50:01  
Job time: 1406 sec

**THIS PAGE BLANK (user)**

---